

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 22.8974 Seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPETGELDSATLKA.....VPLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	258	100.0	707	3	US-08-704-711A-19
2	258	100.0	707	3	US-09-521-220-19
3	258	100.0	707	3	US-09-391-104-20
4	258	100.0	707	4	US-09-949-016-6575
5	258	100.0	708	3	US-08-448-489-16
6	258	100.0	708	4	US-09-689-730-16
7	258	100.0	713	4	US-09-949-016-10629
8	141	54.7	477	3	US-08-704-711A-20
9	141	54.7	477	3	US-08-448-489-15
10	141	54.7	477	3	US-08-281-313-1
11	141	54.7	477	3	US-09-521-220-20
12	141	54.7	477	3	US-09-391-104-21
13	141	54.7	477	4	US-09-689-730-15
14	133	51.6	476	3	US-08-704-711A-21
15	133	51.6	476	3	US-08-448-489-14
16	133	51.6	476	3	US-09-521-220-21
17	133	51.6	476	3	US-09-391-104-22
18	133	51.6	476	4	US-09-949-016-6224
19	133	51.6	476	4	US-09-689-730-14
20	133	51.6	484	4	US-09-949-016-10877
21	117	45.3	471	3	US-09-391-104-25
22	117	45.3	480	4	US-09-949-016-10560
23	115	44.6	136	4	US-09-513-999C-4639
24	115	44.6	663	4	US-09-194-468A-30
25	114	44.2	631	3	US-08-448-489-17
26	114	44.2	631	4	US-09-689-730-17
27	114	44.2	660	3	US-08-704-711A-18

28	114	44.2	660	3	US-09-521-220-18	Sequence 18, Appl
29	114	44.2	660	3	US-09-391-104-19	Sequence 19, Appl
30	114	44.2	660	4	US-09-917-254-89	Sequence 89, Appl
31	114	44.2	660	4	US-09-949-016-6512	Sequence 6512, Ap
32	114	44.2	660	4	US-09-949-016-7937	Sequence 7937, Ap
33	113	43.8	470	3	US-08-068-392-2	Sequence 2, Appl
34	113	43.8	470	3	US-08-396-988-2	Sequence 2, Appl
35	113	43.8	470	3	US-09-391-104-26	Sequence 26, Appl
36	113	43.8	473	4	US-09-949-016-10876	Sequence 10876, A
37	110	42.6	469	3	US-08-704-711A-16	Sequence 16, Appl
38	110	42.6	469	3	US-08-448-489-12	Sequence 12, Appl
39	110	42.6	469	3	US-09-521-220-16	Sequence 16, Appl
40	110	42.6	469	3	US-09-391-104-23	Sequence 23, Appl
41	110	42.6	469	4	US-09-949-016-6223	Sequence 6223, Ap
42	110	42.6	469	4	US-09-689-730-12	Sequence 12, Appl
43	110	42.6	491	4	US-09-949-016-10875	Sequence 10875, A
44	109	42.2	513	4	US-09-862-631-4	Sequence 4, Appl
45	108	41.9	471	4	US-08-994-689C-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-704-711A-19
; Sequence 19, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683.
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 707 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-19

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 2

US-09-521-220-19
 ; Sequence 19, Application US/09521220
 ; Patent No. 639348
 ; GENERAL INFORMATION:
 ; APPLICANT: WILL, Horst
 ; INVENTOR: HINZMANN, Bernd
 ; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
 ; METALLOPROTEASES, THEIR PRODUCTION AND USE
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley & Lardner
 ; STREET: 3000 K Street, N.W., Suite 500
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20007-5109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/521,220
 ; FILING DATE: 08-Mar-2000
 ; CLASSIFICATION: <Unknown>
 ; 21-OCT-1994
 ; 17-MAR-1994

PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/704,711
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: DE 4438838.1
 ; FILING DATE: 21-OCT-1994
 ; APPLICATION NUMBER: DE 4409663.1
 ; FILING DATE: 17-MAR-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: GRANADOS, Patricia D.
 ; REGISTRATION NUMBER: 33,683
 ; REFERENCE/DOCKET NUMBER: 26083/124
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202)672-5300
 ; TELEFAX: (202)672-5399
 ; TELETYPE: 904136

INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 3

US-09-391-104-20

; Sequence 20, Application US/093911104
 ; Patent No. 639371
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Falduto, Michael T.
 ; APPLICANT: Magnuson, Scott R.
 ; APPLICANT: Morgan, Douglas W.
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
 ; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
 ; TITLE OF INVENTION: OF USING SAME
 ; FILE REFERENCE: 6073.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/391,104
 ; PRIOR FILING DATE: 1999-09-07
 ; PRIOR APPLICATION NUMBER: US 08/814,394
 ; PRIOR FILING DATE: 1997-03-11
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 20
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-391-104-20

Query Match 100.0%; Score 258; DB 3; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 4

US-09-949-016-6575
 ; Sequence 6575, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 6575
 ; LENGTH: 707
 ; TYPE: PRT
 ; ORGANISM: Human
 ; US-09-949-016-6575

Query Match 100.0%; Score 258; DB 4; Length 707;
 Best Local Similarity 100.0%; Pred. No. 1.9e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 5

US-08-448-489-16
 ; Sequence 16, Application US/08448489
 ; Patent No. 6184022
 ; GENERAL INFORMATION:
 ; APPLICANT: SEIKI, Motoharu
 ; APPLICANT: SATO, Hiroshi

Amend 2/6/01

APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/08/448,489
CURRENT FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 16
LENGTH: 708
TYPE: PNT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: X = UNKNOWN
OTHER INFORMATION: Description of Unknown Organism: Known Member of
OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-16

Query Match 100.0%; Score 258; DB 3; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.9e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 6
US-09-689-730-16
Sequence 16, Application US/09689730
Patent No. 6825024
GENERAL INFORMATION:
APPLICANT: SEIKI, Motoharu
APPLICANT: SATO, Hiroshi
APPLICANT: SHINAGAWA, Akira
TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
FILE REFERENCE: 55-290P
CURRENT APPLICATION NUMBER: US/09/689,730
CURRENT FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US/08/448,489
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 19
SOFTWARE: Patentin ver. 2.0
SEQ ID NO 16
LENGTH: 708
TYPE: PNT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: X = UNKNOWN
OTHER INFORMATION: Description of Unknown Organism: Known Member of
OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-16

Query Match 100.0%; Score 258; DB 4; Length 708;
Best Local Similarity 100.0%; Pred. No. 1.9e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
Db 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 7
US-09-949-016-10629
Sequence 10629, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10629
LENGTH: 713
TYPE: PRT
ORGANISM: Human
US-09-949-016-10629

Query Match 100.0%; Score 258; DB 4; Length 713;
Best Local Similarity 100.0%; Pred. No. 1.9e-29;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
Db 80 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 126

RESULT 8
US-08-704-711A-20
Sequence 20, Application US/08704711A
Patent No. 6114159
GENERAL INFORMATION:
APPLICANT: WILLY, Horst
APPLICANT: HINZMANN, Bernd
TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
METALLOPROTEASES, THEIR PRODUCTION AND USE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSES: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/704,711A
FILING DATE: 20-NOV-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/DE95/00357
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-704-711A-20

No d's to Prod.
D Products w/
Repl.

Gen out w/ 3 mutations del Ref.
↑
Volutes ← Cl. 3 1-173 No.
Cl. 1
No Comp w/
Mo word
drawing

↑ Same as, only
Cl's to DNA, & Reptable Part.

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVDPDVGHFTFPFGIPKW 109

RESULT 11

US-09-521-220-20
; Sequence 20, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521.220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/704,711
FILING DATE: <Unknown>
APPLICATION NUMBER: DE 4438838.1
FILING DATE: 21-OCT-1994
APPLICATION NUMBER: DE 4409663.1
FILING DATE: 17-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 26083/124
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-521-220-20

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVDPDVGHFTFPFGIPKW 109

RESULT 12

US-09-391-104-21
; Sequence 21, Application US/09391104

; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-21

Query Match 54.7%; Score 141; DB 3; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVDPDVGHFTFPFGIPKW 109

RESULT 13

US-09-689-730-15
; Sequence 15, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 15
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-15

Query Match 54.7%; Score 141; DB 4; Length 477;
Best Local Similarity 62.8%; Pred. No. 2.6e-12;
Matches 27; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGLKW 43
Db 67 MQKFLGLEVTGKLDSDTLVWRKPRCGVDPDVGHFTFPFGIPKW 109

RESULT 14

US-08-704-711A-21
; Sequence 21, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX

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US-08-448-489-14

Query Match          51.6%;      Score 133;   DB 3;   Length 476;
Best Local Similarity 58.1%;    Pred. No. 3.9e-11;
Matches 25; Conservative 6; Mismatches 12; Indels

Qy  1 LKQLSLPETGELDSATLKAVPRCGVDPDGLRFTQTFEGDLKW 43
      :|::||::||::||::||::||::||::||::||::||::||
Db  66 MQKFLGLEVTGKLDTLTLEVMRKRCGVDPDVGHFSSFGMPKW 108

Search completed: May 27, 2005, 06:47:41
Job time : 23.8974 secs
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Query Match 51.6%; Score 133; DB 3; Length 476;

1 LQQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKW 43

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RESULT 15
US-08-448-489-14
; Sequence 14, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE
; FILE REFERENCE: 53-290P
; CURRENT APPLICATION NUMBER: US/08/448,489

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 91.2885 Seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQKQLSLPETGELDSATLKA.....VPLGRFQTFEGDLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	100.0	47	6	ABP97130 Human mat
2	258	100.0	47	6	ABG76316 Human mat
3	258	100.0	47	6	ADQ17091 Human mat
4	258	100.0	432	5	ABP69247 Human pol
5	258	100.0	702	5	ABP69246 Human pol
6	258	100.0	707	2	AAR07077 92-kDa hu
7	258	100.0	707	3	AA558015 Matrix me
8	258	100.0	707	4	AA804611 Amino aci
9	258	100.0	707	4	AAE10432 Human mat
10	258	100.0	707	4	AAE10491 Human mat
11	258	100.0	707	6	ABU56680 Lung canc
12	258	100.0	707	6	ABU56467 Lung canc
13	258	100.0	707	6	AAO16609 Human mat
14	258	100.0	707	6	ABR92116 Human cer
15	258	100.0	707	7	ADL14993 Human typ
16	258	100.0	707	7	ADN39040 Cancer/an
17	258	100.0	707	7	ADN39935 Cancer/an
18	258	100.0	707	8	ADH17067 Human mat
19	258	100.0	707	8	ADJ75581 Marker ge
20	258	100.0	707	8	ADM67186 Human adi
21	258	100.0	707	8	ADN07701 Human mat
22	258	100.0	707	8	ADQ19168 Human sof
23	258	100.0	707	8	ABM82250 Tumour-as
24	258	100.0	707	8	ADP54466 Human PRO
25	258	100.0	707	8	ADP23624 PRO polyp

ALIGNMENTS

RESULT 1

ABP97130

ID ABP97130 standard; peptide; 47 AA.

XX AC ABP97130;

XX XX 24-JUN-2003 (first entry)

DE Human matrix metalloproteinase 9 cleavage region peptide SEQ ID NO:8.

XX Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumour; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.

XX Homo sapiens.

XX WO2003018748-A2.

XX PD 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Weart IF;

XX WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

XX The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological and dermatological activities. (I) can be

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (1) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;
 Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||

RESULT 2

ABG76316
 ID ABG76316 standard; protein; 47 AA.

AC ABG76316;

XX DT 10-MAY-2003 (first entry)

DE Human matrix metalloproteinase (MMP) peptide inhibitor #8.

XX Human; peptide inhibitor; matrix metalloproteinase-9; MMP-9;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.

XX Homo sapiens.

XX WO2003016520-A1.

XX PD 27-FEB-2003.

XX PF 15-AUG-2002; 2002WO-US026198.

XX PR 16-AUG-2001; 2001US-0312726P.

XX PR 21-DEC-2001; 2001US-00032376.

XX PR 21-MAY-2002; 2002US-00153185.

XX PA (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX PI Quirk S, Malik S, Villanueva JM;

XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for stimulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 6; Length 47;

Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||

RESULT 3

ADQ17091
 ID ADQ17091 standard; peptide; 47 AA.

XX AC ADQ17091;

XX DT 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-9 (MMP9) cleavage region peptide.

XX Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

XX US2004127421-A1.

XX PD 01-JUL-2004.

XX PF 30-DEC-2002; 2002US-00335207.

XX PR 30-DEC-2002; 2002US-00335207.

XX PA (MALI/) MALIK S.

XX PA (QUIR/) QUIRK S.

XX PI Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 8; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 47 AA;

Query Match 100.0%; Score 258; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 3.3e-29;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 Db 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||

RESULT 4

ABP69247
 ID ABP69247 standard; protein; 432 AA.

XX AC ABP69247;

XX DT 20-JAN-2003 (first entry)

XX

DE XX Human polypeptide SEQ ID NO 1294.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.

XX Homo sapiens.

XX WO200270539-A2. = US 6,783,969 B1

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US0005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX WPI; 2002-759812/82.
 DR N-PSDB; ABZ11464.

XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.

XX Claim 9; SEQ ID NO 1294; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 432 AA;

Query Match 100.0%; Score 258; DB 5; Length 432;
 Best Local Similarity 100.0%; Pred. No. 5e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
 DB 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 5
 ABP69246
 ID ABP69246 standard; protein; 702 AA.
 XX AC ABP69246;
 XX 20-JAN-2003 (first entry)
 DT

DE XX Human polypeptide SEQ ID NO 1293.

XX Human; genome mapping; gene therapy; food supplement; virus; fungus;
 KW cell-proliferative disorder; neurodegenerative disease; bacterial;
 KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
 KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
 KW arthritis; cytostatic; immunomodulator; neurotropic; neuroprotective;
 KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
 KW haemostatic; vulnary; fungicide; antibacterial; virucide; protozoacide;
 KW antiarthritic.

XX Homo sapiens.

XX WO200270539-A2. = US 6,783,969 B1

XX 12-SEP-2002.

XX 05-MAR-2002; 2002WO-US0005095.

XX 05-MAR-2001; 2001US-00799451.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
 PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
 PI Wehrman T, Wang J, Wang D, Drmanac RT;
 XX WPI; 2002-759812/82.
 DR N-PSDB; ABZ11463.

XX New polynucleotides comprising sequences assembled from expressed
 PT sequence tags (ESTs), useful for treating cell-proliferative,
 PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
 PT or coagulation disorders.

XX Claim 9; SEQ ID NO 1293; 1012pp + Sequence Listing; English.

XX The invention relates to an isolated polynucleotide (I) comprising a
 CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
 CC ABZ12066) or their mature protein coding portion, active domain coding
 CC protein or complementary sequences. The polynucleotides are useful for
 CC identifying expressed genes or for physical mapping of human genome. The
 CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
 CC markers, as a food supplement, for generating antibodies, in medical
 CC imaging, screening and diagnostic assays and for treating cell-
 CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
 CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
 CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
 CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
 CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
 CC arthritis, etc. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 702 AA;

Query Match 100.0%; Score 258; DB 5; Length 702;
 Best Local Similarity 100.0%; Pred. No. 9.1e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
 DB 74 LQKLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 6
 AAR07077
 ID AAR07077 standard; protein; 707 AA.
 XX AC AAR07077;
 XX 25-MAR-2003 (revised)
 DT 19-FEB-1991 (first entry)

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XX DE 92-kDa human type IV collagenase gene product.
XX KW Epidermal growth factor; EGF; interleukin 1; IL-1; tumour TPA.
XX OS Homo sapiens.
XX FH Key
XX FT Protein
XX FT /label= Mature protein
XX FT Active-site
XX FT /label= Glycosylation site
XX FT Active-site
XX FT /label= Glycosylation site
XX FT Active-site
XX FT /label= Glycosylation site
XX PN EP398859-A.
XX XX
XX PD 22-NOV-1990.
XX PF 14-MAY-1990; 90EP-00870069.
XX PR 15-MAY-1989; 89US-00352078.
XX PA (UNIW ) UNIV WASHINGTON.
XX PI Goldberg GI, Eisen AZ;
XX DR WPI; 1990-350579/47.
XX DR N-PSDB; AAQ06554.
XX XX
XX FT New 92-kD type IV collagenase and cDNA - from SV-40 transformed foetal
XX FT lung fibroblasts.
XX PS Claim 1; Fig 3; 21pp; English.
XX CC SV40 transformed foetal lung fibroblasts may be used to produce type IV
XX CC collagenase, totally glycosylated at three sites. The enzyme is induced
XX CC by EGF, IL-2 and the tumour promoter, 12-O-tetradecanoyl- phorbol acetate
XX CC (TPA) and has therapeutic activity, being able to digest native type IV
XX CC and V collagen. (Updated on 25-MAR-2003 to correct PA field.)
XX XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 2; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 7
AAY58015
ID AAY58015 standard; protein; 707 AA.
XX AC
XX AC AAY58015;
XX DT 28-FEB-2000 (first entry)
XX DE
XX DE Matrix metalloproteinase-9 (MMP-9) amino acid sequence.
XX KW Matrix metalloproteinase-9; MMP-9; polymorphism; endopeptidase; detect;
XX KW inflammatory disease; diagnose; atherosclerosis; tumour; metastasis;
XX KW neurological disease; multiple sclerosis; arthritis; human.
XX OS Homo sapiens.
XX XX
XX PN WO957315-A2.
XX XX
XX PD 11-NOV-1999.

XX PF 07-MAY-1999; 99WO-GB001447.
XX PR 07-MAY-1998; 98GB-00009764.
XX PA (ISIS-) ISIS INNOVATION LTD.
XX PI Zhang BP, Ye S, Henney A;
XX FT WPI; 2000-052977/04.
XX DR N-PSDB; AA245145.
XX PT Detection of matrix metalloprotease 9 gene polymorphisms for diagnosis or
XX PT prognosis of diseases characterized by metalloproteinase mediated
XX PT remodelling.
XX PS Example 1; Fig 1; 29pp; English.
XX CC This is the human matrix metalloproteinase-9 (MMP-9) amino acid sequence.
XX CC MMP-9 is a zinc-dependent endopeptidase, and is located on chromosome 20.
XX CC MMP activity is associated with inflammatory diseases and MMP-9 is
XX CC implicated in the pathology of multiple sclerosis. Certain polymorphic
XX CC sequences in the MMP-9 promoter, coding sequence and 3' untranslated
XX CC region of the human MMP-9 gene can affect the severity of
XX CC atherosclerosis. The invention relates to the presence or absence of one
XX CC variant form of a MMP-9 gene polymorphism (-1562 Cytosine/Threonine),
XX CC detection of this polymorphism using oligonucleotides AA245137-245140 can
XX CC be used for disease prognosis. The invention shows that the MMP-9 C-1562T
XX CC polymorphism is a regulatory functional polymorphism. The methods and
XX CC oligonucleotides are used to detect polymorphisms in the MMP-9 gene. They
XX CC are useful for the diagnosis and prognosis of diseases characterized by
XX CC metalloproteinase mediated remodelling, such as atherosclerosis, tumour
XX CC invasion and metastasis, inflammatory disease, and neurological diseases,
XX CC particularly those involving demyelination such as multiple sclerosis,
XX CC and arthritic disease. Proteins encoded by the MMP-9 gene variants may be
XX CC used for screening compounds that bind specifically to a molecule encoded
XX CC by one variant of a polymorphic sequence, thus identifying compounds
XX CC which modulate the activity of the enzyme. Such compounds can then be
XX CC used for rational drug design
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
DB 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 8
AAB84611
ID AAB84611 standard; protein; 707 AA.
XX AC
XX AC AAB84611;
XX DT 05-SEP-2001 (first entry)
XX DE
XX DE Amino acid sequence of matrix metalloproteinase-9.
XX KW Growth factor; protein inhibitor; protease; damaged tissue;
XX KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
XX KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
XX KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
XX KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
XX KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
XX KW vascular endothelial growth factor; urokinase plasminogen activator;
XX KW dermal ulcer; wound.
XX OS Homo sapiens.
XX XX
XX PN WO200149309-A2.

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XX PD 12-JUL-2001.
XX PF 21-DEC-2000; 2000WO-IB001935.
XX PR 29-DEC-1999; 99GB-00030768.
XX PA (PF1Z ) PFIZER LTD.
XX PA (PF1Z ) PFIZER INC.
XX PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX WPI; 2001-418351/44.
XX DR N-PSDB; AAH28226.
XX PT Composition for the treatment of damaged tissue i.e. chronic wounds and
XX PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX PT factor.
XX PS Disclosure; Page 557; 572pp; English.
XX CC The specification describes a pharmaceutical composition, comprising a
XX CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
XX CC inhibits the action of at least one specific adverse protein, i.e. a
XX CC protease, that is upregulated in a damaged tissue such as a wound
XX CC environment. Growth factors which are included in the composition of the
XX CC invention are platelet-derived growth factor (PDGF), fibroblast growth
XX CC factor (FGF), connective tissue derived growth factor (CTGF),
XX CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
XX CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
XX CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
XX CC and chrysalin. Inhibitors which are included in the composition of the
XX CC invention include inhibitors of urokinase-type plasminogen activator
XX CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
XX CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
XX CC The present sequence represents a human MMP-9, and is used to produce the
XX CC composition of the invention
XX SQ Sequence 707 AA;
Query Match 100.0%; Score 258; DB 4; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120
RESULT 9
AAE10432
ID AAE10432 standard; protein; 707 AA.
XX AC AAE10432;
XX DT 10-DEC-2001 (first entry)
XX DE Human matrix metalloproteinase-9 (MMP-9) protein.
XX KW Human; matrix metalloproteinase; MMP-9; hair growth; antisense therapy;
XX KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT /label= Signal_peptide
XX FT Protein 22..707
XX FT /label= Mature_MMP_2_protein
XX FT Domain 97..103
XX FT /label= Cysteine_switch_domain
XX FT Domain 168..192
XX FT /note= "Zinc and calcium binding domain"
XX
XX PD 12-JUL-2001.
XX PF 21-SEP-2001.
XX PR 06-MAR-2001; 2001WO-US007167.
XX PR 06-MAR-2000; 2000US-0187196P.
XX PA (DARW-) DARWIN MOLECULAR CORP.
XX PA (SCHA/) SCHATZMAN R.
XX PI Fajardo M, Wang K, Smith R, Moss P;
XX WPI; 2001-582276/65.
XX PT Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
XX PT proteins encoded by them whose inhibition is useful for modulation of
XX PT hair growth in mammals.
XX PS Example 2; Fig 3; 119pp; English.
XX CC The present sequence is human matrix metalloproteinase (MMP)-9 protein
XX CC used in the exemplification of the invention. MMP-25 DNA is located on
XX CC chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX CC dependent endopeptidases that function extracellularly to degrade
XX CC proteins typically found in the extracellular matrix. MMP-25 is expressed
XX CC in skin cells of mammals, particularly in breast cells and hair
XX CC follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX CC encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX CC sample and identifying a sequence that hybridises in the nucleic acid
XX CC sample. The identification step involves performing polymerase chain
XX CC reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX CC useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX CC to modulate hair growth and breast cancer in a mammal
XX SQ Sequence 707 AA;
Query Match 100.0%; Score 258; DB 4; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120
RESULT 10
AAB20491
ID AAB20491 standard; protein; 707 AA.
XX AC AAB20491;
XX DT 21-JUN-2001 (first entry)
XX DE Human matrix metalloproteinase-9 (MMP-9).
XX KW Matrix metalloproteinase-9; MMP-9; human; pain; analgesic;
XX KW nerve tissue damage; stroke; haemorrhage; reperfusion injury;
XX KW cerebral ischaemia; cerebral infarction; narcotic tolerance;
XX KW narcotic withdrawal.
XX OS Homo sapiens.
XX PN WO200126671-A1.
XX PD 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-US027949.
XX PR 12-OCT-1999; 99US-0158787P.
XX PA (SMIK ) SMITHKLINE BEECHAM CORP.

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PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX Romanic Arnold A, Barone FC, Bingham S;
 XX WPI; 2001-290654/30.
 DR N-PSDB; AAF30808.
 XX Polypeptide for the treatment of pain and the reduction of tissue damage
 PT comprises an inhibitor of human matrix metalloproteinase.
 XX Claim 1; Fig 4; 61pp; English.
 XX The present sequence is that of human matrix metalloproteinase-9 (MMP-9),
 CC previously known as 92 kDa gelatinase and gelatinase B. MMP-9 is capable
 CC of degrading the extracellular matrix components of the basement
 CC membrane. The invention relates to methods for treating pain in a patient
 CC by administering a dual inhibitor of MMP-9 and MMP-2 (see AAB20490). The
 CC administration of an inhibitor of MMP-9 is useful for treating nerve
 CC tissue damage (claimed), where the patient is suffering from a disease or
 CC disorder selected from stroke, haemorrhage, reperfusion injury, cerebral
 CC ischaemia and cerebral infarction (claimed). The method is useful for
 CC treating a disease, disorder or nerve tissue damage selected from
 CC enhanced or exaggerated sensitivity to acute pain, burn pain, atypical
 CC facial pain, neuropathic pain, back pain, complex regional pain syndrome
 CC I and II, arthritic pain, sports injury pain, pain related to virus
 CC infection, post-herpetic neuralgia, phantom limb pain, labour pain,
 CC cancer pain, post-chemotherapy pain, post-operative pain, post-stroke
 CC pain, physiological pain, inflammatory pain, acute inflammatory
 CC conditions/visceral pain, neuralgia, painful diabetic retinopathy,
 CC traumatic nerve injury, and tolerance to narcotics or withdrawal from
 CC narcotics (claimed). MMP-9 polypeptides can also be used to screen for
 CC agonist or antagonist (inhibitor) compounds
 XX Sequence 707 AA;
 SQ

Query Match 100.0%; Score 258; DB 4; Length 707;
 Best Local Similarity 100.0%; Pred. No. 9.2e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 DB 74 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 11
 ABUS6680
 ID ABUS6680 standard; protein; 707 AA.
 XX
 AC ABUS6680;
 DT
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polypeptide #273.
 XX
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS
 PN WO200286443-A2.
 XX
 XX 31-OCT-2002.
 PD
 PF 18-APR-2002; 2002WO-US012476.
 XX
 XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.
 PR 09-NOV-2001; 2001US-0339245P.
 PR 13-NOV-2001; 2001US-0350666P.
 PR 29-NOV-2001; 2001US-0334370P.

PA 12-APR-2002; 2002US-0372246P.
 XX (EOSB-) EOS BIOTECHNOLOGY INC.
 XX Aziz N, Murray R;
 XX WPI; 2003-093161/08.
 DR N-PSDB; ABX76409.
 XX Detecting a lung cancer-associated transcript in a cell from a patient
 PT for treating lung cancer, by contacting a biological sample from the
 PT patient with a polynucleotide that exhibits increased or decreased
 PT expression in lung cancer.
 XX Claim 27; Page 398; 453pp; English.
 XX The invention relates to a method for detecting a lung cancer-associated
 CC transcript in a cell from a patient, comprising contacting a biological
 CC sample from the patient with a polynucleotide that selectively hybridises
 CC to a sequence that is at least 80 % identical to a gene that exhibits
 CC increased or decreased expression in lung cancer samples. Lung cancer-
 CC associated polynucleotides and polypeptides are used for identifying a
 CC compound that modulates a lung cancer-associated polypeptide, for
 CC inhibiting proliferation of a lung cancer-associated cell to treat lung
 CC cancer in a patient and for treating a mammal having lung cancer by
 CC administering a modulatory compound identified. The methods are useful
 CC for treating lung cancer, such as small cell lung cancer, non-small cell
 CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
 CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
 CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
 CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
 CC for diagnostic purposes and as targets for screening for therapeutic
 CC compounds that modulate lung cancer, such as antibodies. Sequences
 CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
 CC invention
 XX Sequence 707 AA;
 SQ

Query Match 100.0%; Score 258; DB 6; Length 707;
 Best Local Similarity 100.0%; Pred. No. 9.2e-28;
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 47
 |||||
 DB 74 LQKQLSLPETGELDSATLKAMETPRCGVDPDLGRFQTFEGDLKWHHN 120
 |||||

RESULT 12
 ABUS6467
 ID ABUS6467 standard; protein; 707 AA.
 XX
 AC ABUS6467;
 DT
 DT 02-APR-2003 (first entry)
 XX
 DE Lung cancer-associated polypeptide #60.
 XX
 XX Lung cancer-associated polypeptide; cytostatic; emphysema;
 KW antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
 KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
 KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
 KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
 XX Unidentified.
 OS
 PN WO200286443-A2.
 XX
 XX 31-OCT-2002.
 PD
 PF 18-APR-2002; 2002WO-US012476.
 XX
 XX 18-APR-2001; 2001US-0284770P.
 PR 10-MAY-2001; 2001US-0290492P.


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PR 09-NOV-2001; 2001US-0339245P.
PR 13-NOV-2001; 2001US-0350666P.
PR 29-NOV-2001; 2001US-0334370P.
PR 12-APR-2002; 2002US-0372246P.
XX (EOSB-) EOS BIOTECHNOLOGY INC.
PA Aziz N, Murray R;
PI WPI; 2003-093161/08.
XX N-PSDB; ABX76189.
XX Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
XX Claim 27; Page 236; 453pp; English.
XX
XX The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABUS6408-ABUS6745 represent lung cancer-associated polypeptides of the
CC invention
XX
SQ Sequence 707 AA;
Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. NO. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 13
AAO16609
ID AAO16609 standard; protein; 707 AA.
XX
XX AAO16609;
AC
XX
XX 08-MAY-2003 (first entry)
DT
XX
XX Human matrix metalloproteinase 9 (MMP9) gelatinase protein.
DE
XX
XX Human; enzyme; crystalline polypeptide; matrix metalloproteinase 9; MMP9;
KW gelatinase; metalloproteinase mediated disease; drug design; arthritis;
KW three-dimensional structure; MMP9 inhibitor; tumour growth;
KW cancer metastasis; osteoarthritis; atherosclerosis; restenosis;
KW periodontitis; multiple sclerosis; glomerulonephritis; MMP9 modulator;
KW graft-versus-host disease; non-insulin dependent diabetes.
XX
XX Homo sapiens.
OS
XX
XX WO2003002729-A1.
PN
XX
XX 09-JAN-2003.
PD
XX
XX

```

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PF 24-JUN-2002; 2002WO-SE001266.
PR 27-JUN-2001; 2001SE-00002298.
XX (ASTR ) ASTRAZENECA AB.
XX Jepson H, Minshull C, Pauprit R, Rowsell S;
PI WPI; 2003-201502/19.
XX
XX Novel crystalline form of a polypeptide corresponding to the catalytic
PT domain of matrix metalloproteinase 9 protein, useful for selecting or
PT designing chemical modulators which are used for treating diabetes,
PT cancer, arthritis.
XX
XX Disclosure; Fig 7; 227pp; English.
XX
XX The invention comprises a crystalline form of a polypeptide corresponding
CC to the catalytic domain of matrix metalloproteinase 9 (MMP9) protein - a
CC gelatinase. The crystalline polypeptide of the invention is useful for
CC treating a metalloproteinase mediated disease or condition in a warm-
CC blooded animal. The crystalline polypeptide is also useful for
CC determining the three-dimensional structure of the MMP9 catalytic domain
CC to high resolution. The three-dimensional structure of the MMP9 catalytic
CC domain is useful for rational drug design, and the atomic coordinates of
CC the catalytic domain of MMP9 are useful for selecting or designing
CC chemical modulators (preferably inhibitors) of MMP9. The crystalline
CC polypeptide of the invention is useful in the treatment of a
CC metalloproteinase mediated disease or condition, such as: tumour growth;
CC metastasis in cancer; arthritis; osteoarthritis; atherosclerosis;
CC restenosis; periodontitis; multiple sclerosis; glomerulonephritis; graft-
CC versus-host disease; and non-insulin dependent diabetes. The present
CC amino acid sequence represents a human matrix metalloproteinase 9 (MMP9)
CC protein
XX
XX Sequence 707 AA;
Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. NO. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 47
DB 74 LQKQLSLPETGELDSATLKAMRTPCGVPDLGRFQTPEGDLKWHHN 120

RESULT 14
ABR92116
ID ABR92116 standard; protein; 707 AA.
XX
XX ABR92116;
AC
XX
XX 10-SEP-2003 (first entry)
DT
XX
XX Human cervical cancer cell marker protein SEQ ID NO:142.
DE
XX
XX Human; cervical cancer; cervical cancer marker; cancer therapy;
KW detection; gene therapy; vaccine.
XX
XX Homo sapiens.
OS
XX
XX WO2002101075-A2.
PN
XX
XX 19-DEC-2002.
PD
XX
XX 12-JUN-2002; 2002WO-US018638.
PF
XX
XX 13-JUN-2001; 2001US-0298155P.
PR 13-JUN-2001; 2001US-0298159P.
PR 14-NOV-2001; 2001US-0335936P.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
XX

```

PI Schlegel R, Chen Y, Zhao X, Monahan JE, Kamatkar S;
PI Gannavarapu M, Glatt K, Hoersch S;
XX
XX WPI; 2003-156967/15.
XX N-PSDB; ACFI2899.
XX
XX New isolated nucleic acid molecule useful for detecting, characterizing,
PT preventing and treating human cervical cancers, in various prognostic and
PT diagnostic assays, in pharmacogenomics and in monitoring clinical trials.
XX
XX Claim 4; Page 294-295; 386pp; English.
XX
XX ACFI2828 to ACFI2947 encode the human cervical cancer marker proteins (I)
CC given in ABR92047 to ABR92164. A higher level of expression of (I) than
CC normal indicates the presence of cervical cancer. Also described: (I) a
CC vector (II) containing (I); (2) a host cell (III) containing (I); and (3)
CC assessing (M1) whether a patient is afflicted with cervical cancer,
CC comprising comparing the level of expression of a marker in a patient's
CC sample, and the normal level of expression of the marker in a control non
CC -cervical cancer sample, where a significant increase in the level of
CC expression of the marker in the patient's sample relative to that in the
CC control sample is an indication that the patient is afflicted with
CC cervical cancer. (I) has cytostatic activity, and can be used in gene
CC therapy and in vaccines. (I) is useful in detecting, characterizing,
CC preventing and treating human cervical cancers. (I) may also be used in
CC various prognostic and diagnostic assays, pharmacogenomics and in
CC monitoring clinical trials
XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 6; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 15
ADL14993
ID ADL14993 standard; protein; 707 AA.
XX
XX AC ADL14993;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human type IV collagenase protein for cancer treatment.
XX
XX KW cytostatic; gene therapy; binding moiety; medicine; imaging; diagnosis;
XX KW prognosis; mantle cell lymphoma; cancer.
XX
XX OS Homo sapiens.
XX
XX PN WO2003068268-A2.
XX
XX PD 21-AUG-2003.
XX
XX PF 13-FEB-2003; 2003WO-EP001461.
XX
XX PR 14-FEB-2002; 2002GB-00003480.
XX PR 29-JUN-2002; 2002GB-00015095.
XX
XX PA (BIOI-) BIOINVENT INT AB.
XX
XX PI Ek S, Borrebaeck CAK, Ehinger M;
XX
XX DR WPI; 2003-697496/66.
XX DR N-PSDB; ADL14994.
XX
XX New compound for treating, imaging, diagnosing or prognosing mantle cell
PT lymphoma, comprises a binding moiety (e.g. antibody) that binds to a
PT protein (e.g. human autotaxin polypeptide), and a further moiety (e.g.

PT nucleic acid).
XX
XX PS Disclosure; SEQ ID NO 5; 342pp; English.
XX
XX CC The invention relates to a compound comprising a binding moiety which
CC selectively binds to a protein or polypeptide listed in the specification
CC (e.g. human autotaxin polypeptide or human CD24 signal transducer
CC polypeptide), and a further moiety. The compound is useful in medicine or
CC in the treatment, imaging, diagnosis or prognosis of mantle cell
CC lymphomas (MCL). It is used in preparing a medicament for treating MCL, a
CC diagnostic or prognostic agent for MCL, or an agent for imaging MCL cells
CC in the body of an individual. This sequence corresponds to one of the
CC polypeptides of the invention.
XX
XX SQ Sequence 707 AA;

Query Match 100.0%; Score 258; DB 7; Length 707;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
|||||
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

Search completed: May 27, 2005, 06:52:53
Job time : 95.2885 secs

Result No.	Query			Description		
	Score	Match	Length	ID		
1	258	100.0	47	14	US-10-219-329-8	Sequence 8, Appli
2	258	100.0	47	14	US-10-153-185-8	Sequence 8, Appli
3	258	100.0	47	14	US-10-219-561-8	Sequence 8, Appli
4	258	100.0	47	16	US-10-032-376A-8	Sequence 8, Appli
5	258	100.0	47	16	US-10-335-207-8	Sequence 8, Appli
6	258	100.0	707	9	US-09-391-104-20	Sequence 20, Appl
7	258	100.0	707	9	US-09-801-196-36	Sequence 36, Appl
8	258	100.0	707	14	US-10-171-311-142	Sequence 142, App
9	258	100.0	707	14	US-10-301-822-132	Sequence 132, App
10	258	100.0	707	14	US-10-131-985-33	Sequence 33, Appl
11	258	100.0	707	15	US-10-295-027-358	Sequence 358, App
12	258	100.0	707	15	US-10-295-027-1253	Sequence 1253, Ap
13	258	100.0	707	15	US-10-440-464-66	Sequence 66, Appl

```
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47
Db 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47

RESULT 3
US-10-219-561-8
; Sequence 8, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-8

Query Match      100.0%; Score 258; DB 14; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47
Db 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47

RESULT 4
US-10-032-376A-8
; Sequence 8, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
```

```
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47
Db 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47

RESULT 5
US-10-335-207-8
; Sequence 8, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 47
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-8

Query Match      100.0%; Score 258; DB 16; Length 47;
Best Local Similarity 100.0%; Pred. No. 9.2e-28;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47
Db 1 LQQLSLPETGELDSATLKAMRTPRCGVPLGRFQTFEGDLKWHHN 47

RESULT 6
US-09-391-104-20
; Sequence 20, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-20

Query Match      100.0%; Score 258; DB 9; Length 707;
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Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 7
US-09-801-196-36
; Sequence 36, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT APPLICATION NUMBER: US/09/801.196
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-36

Query Match 100.0%; Score 258; DB 9; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 8
US-10-171-311-142
; Sequence 142, Application US/10171311
; Publication No. US20030087270A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Yan
; APPLICANT: Schlegel, Robert
; APPLICANT: Zhao, Xumei
; APPLICANT: Monahan, John
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Glatt, Karen
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Hoerish, Sebastian
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND THERAPY
; TITLE OF INVENTION: OF CERVICAL CANCER
; FILE REFERENCE: MRI-035
; CURRENT APPLICATION NUMBER: US/10/171.311
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US 60/298,159
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,155
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/335,936
; PRIOR FILING DATE: 2001-11-14
; NUMBER OF SEQ ID NOS: 238
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-171-311-142

Query Match 100.0%; Score 258; DB 14; Length 707;

Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 9
US-10-301-822-132
; Sequence 132, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301.822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-132

Query Match 100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
Db 74 LQQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120

RESULT 10
US-10-131-985-33
; Sequence 33, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 707
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-33

Query Match      100.0%; Score 258; DB 14; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
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RESULT 11
US-10-295-027-358
; Sequence 358, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 358
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-358

Query Match      100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
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Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
   |||||

RESULT 12
US-10-295-027-1253
; Sequence 1253, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 358
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-358

Query Match      100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
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RESULT 13
US-10-440-464-66
; Sequence 66, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
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; Sequence 1253, Application US/10295027
; Publication No. US20030232350A1
; GENERAL INFORMATION:
; APPLICANT: Afar, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Ginsberg, Wendy M.
; APPLICANT: Gish, Kurt C.
; APPLICANT: Glynn, Richard
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H.
; APPLICANT: Murray, Richard
; APPLICANT: Watson, Susan R.
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-012500US
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: US 09/663,733
; PRIOR FILING DATE: 2000-09-15
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/335,394
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: US 60/332,464
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/334,393
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: US 60/340,376
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1253
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-295-027-1253

Query Match      100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 47
   |||||
Db 74 LOKQLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTFEGDLKWHHN 120
   |||||

RESULT 13
US-10-440-464-66
; Sequence 66, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
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; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-66

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 120

RESULT 14
US-10-447-315-7
; Sequence 7, Application US/10447315
; Publication No. US20040071687A1
; GENERAL INFORMATION:
; APPLICANT: Rafii, Shahin
; APPLICANT: Heissig, Beate
; APPLICANT: Hattori, Koichi
; APPLICANT: Cornell Research Foundation, Inc.
; TITLE OF INVENTION: Adult Stem Cell Recruitment
; FILE REFERENCE: 1576.006US1
; CURRENT APPLICATION NUMBER: US/10/447,315
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US 60/383,658
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-315-7

Query Match 100.0%; Score 258; DB 15; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 120

RESULT 15
US-10-480-621-2
; Sequence 2, Application US/10480621
; Publication No. US20040175817A1
; GENERAL INFORMATION:
; APPLICANT: Jepson, Holly
; APPLICANT: Minshull, Claire
; APPLICANT: Paupit, Richard
; APPLICANT: Rowsell, Sian
; TITLE OF INVENTION: A CRYSTALLISED CATALYTIC DOMAIN OF MATRIX
; TITLE OF INVENTION: METALLOPROTEINASE 9 (MMP9) AND THE USE OF
; TITLE OF INVENTION: ITS THREE DIMENSIONAL STRUCTURE TO DESIGN
; TITLE OF INVENTION: MMP9 MODULATORS
; FILE REFERENCE: 06275-377US1
; CURRENT APPLICATION NUMBER: US/10/480,621
; CURRENT FILING DATE: 2003-12-12
; PRIOR APPLICATION NUMBER: PCT/SE02/01266

; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: SE 0102298-7
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 707
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-480-621-2

Query Match 100.0%; Score 258; DB 16; Length 707;
Best Local Similarity 100.0%; Pred. No. 2e-26;
Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 47
Db 74 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHN 120

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 17.7756 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-8
Perfect score: 258
Sequence: 1 LKQLSLPETGELDSATLKA.....VPDLGRFQTFEGDLKWHHNN 47
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	258	100.0	702	1 A34458	gelatinase B (EC 3
2	236	91.5	708	2 JC4364	gelatinase B (EC 3
3	235	91.1	707	1 A53796	gelatinase B (EC 3
4	233	90.3	708	2 J62907	gelatinase B (EC 3
5	226	87.6	712	1 I46031	gelatinase B (EC 3
6	213.5	82.8	730	1 I52580	gelatinase B (EC 3
7	213.5	82.8	730	2 JC1456	gelatinase B (EC 3
8	141	54.7	477	1 KCHUS1	stromelysin 1 (EC
9	138	53.5	478	1 KCRBS1	stromelysin 1 (EC
10	134	51.9	475	1 KCRTHH	stromelysin 1 (EC
11	133	51.6	476	1 JC6505	stromelysin 2 (EC
12	133	51.6	476	1 KCHUS2	stromelysin 2 (EC
13	133	51.6	477	1 KCRS22	stromelysin 2 (EC
14	133	51.6	477	1 KCRS21	stromelysin 1 (EC
15	121	46.9	472	2 S29243	interstitial colla
16	120	46.5	662	2 S70365	gelatinase A (EC 3
17	118	45.7	466	2 A23685	interstitial colla
18	117	45.3	471	2 A53711	collagenase 3 (EC
19	116	45.0	267	2 A57490	matrilysin (EC 3.4
20	115	44.6	663	1 S46492	gelatinase A (EC 3
21	114	44.2	660	1 A28153	gelatinase A (EC 3
22	114	44.2	662	2 A42496	gelatinase A (EC 3
23	114	44.2	662	2 S34780	gelatinase A (EC 3
24	113	43.8	470	2 A49499	metalloelastase HM
25	110	42.6	469	1 KCHUI	interstitial colla
26	108	41.9	82	2 PKW052	pro-matrix metallo
27	108	41.9	483	2 JC5743	matrix metalloprot
28	106	41.1	267	1 KCHUM	matrilysin (EC 3.4
29	104.5	40.5	582	2 I84471	matrix metalloprot

30 103 39.9 468 1 KCRBI interstitial colla
31 100.5 39.0 582 2 I38028 matrix metalloprot
32 100 38.8 467 1 KCHUN neutrophil collage
33 99 38.4 469 1 KCPGI interstitial colla
34 98 38.0 469 1 KCBOT interstitial colla
35 97.5 37.8 582 2 I48673 matrix metalloprot
36 96 37.2 521 2 T37252 probable matrix me
37 92 35.7 364 2 E71433 macrophage elastas
38 92 35.7 462 2 A42401 matrix metalloprot
39 91 35.3 616 2 JC7776 probable metallopr
40 88 34.1 305 2 T08836 metalloproteinase
41 85.5 33.1 341 2 T51957 probable metallopr
42 85.5 33.1 342 2 G84885 matrix metalloprot
43 84.5 32.8 669 2 I38029 matrix metalloprot
44 83.5 32.4 378 2 E96724 hypothetical prote
45 80 31.0 587 2 S12805 envlysin (EC 3.4.

ALIGNMENTS

RESULT 1

A34458
Gelatinase B (EC 3.4.24.35) precursor - human
N;Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9 (MMP-9)
C;Species: Homo sapiens (man)
C;Date: 03-Aug-1992 #sequence revision 07-Apr-1994 #text change 09-Jul-2004
C;Accession: A34458; A41166; A42253; A45114; B48417; A61385; A516097; S59488
R;Wilhelm, S.M.; Collier, I.E.; Marmer, B.L.; Eisen, A.Z.; Grant, G.A.; Goldberg, G.I.
J. Biol. Chem. 264, 17213-17221, 1989
A;Title: SV40-transformed human lung fibroblasts secrete a 92-kDa type IV collagenase wh
A;Reference number: A34458; MUID:90008879; PMID:2551898
A;Accession: A34458
A;Molecule type: mRNA
A;Residues: 1-11, 'L', 'I', 'S', 'R', '669-707 <WIL>
A;Cross-references: UNIPROT:P14780; GB:J05070; NID:gl77204; PIDN:AA51539.1; PID:gl77205
R;Huhtala, P.; Tuuttila, A.; Chow, L.T.; Lohi, J.; Keski-Oja, J.; Tryggvason, K.
J. Biol. Chem. 266, 16485-16490, 1991
A;Title: Complete structure of the human gene for 92-kDa type IV collagenase. Divergent
A;Reference number: A41166; MUID:91358433; PMID:1653238
A;Accession: A41166
A;Molecule type: DNA
A;Residues: 1-49;121-127;171-177;214-220;272-278;330-336;389-395;439-542;582-587;631-637
A;Cross-references: GB:M68343; GB:M68344; GB:M68345; GB:M68346; GB:M68347; GB:M68348; GB
A;Note: the authors translated the codon CTC for residue 276 as Lys
R;Ogata, Y.; Engild, J.J.; Negase, H.
J. Biol. Chem. 267, 3581-3584, 1992
A;Title: Matrix metalloproteinase 3 (stromelysin) activates the precursor for the human
A;Reference number: A42253; MUID:92156083; PMID:1371271
A;Accession: A42253
A;Molecule type: protein
A;Residues: 20-34;60-71;107-118 <OGA>
R;Okada, Y.; Gonoji, Y.; Naka, K.; Tomita, K.; Nakanishi, I.; Iwata, K.; Yamashita, K.; I
J. Biol. Chem. 267, 21712-21719, 1992
A;Title: Matrix metalloproteinase 9 (92-kDa gelatinase/type IV collagenase) from HT 1080
A;Reference number: A45114; MUID:93016125; PMID:1400481
A;Accession: A45114
A;Molecule type: protein
A;Residues: 20-32 <OKA>
A;Experimental source: HT 1080 fibrosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:119576)
A;Accession: B45114
A;Molecule type: protein
A;Residues: 94-111 <OK2>
A;Experimental source: HT 1080 fibrosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIP:116742)
A;Note: amino ends of the proenzyme and two activated forms
R;Van Ranst, M.; Norga, K.; Masure, S.; Proost, P.; Vandekerckhove, F.; Auwerx, J.; Van
Cytokine 3, 231-239, 1991
A;Title: The cytokine-protease connection: identification of a 96-kD THP-1 gelatinase an
A;Reference number: A48417; MUID:91355647; PMID:1653055
A;Accession: B48417

A;Cross-references: UNIPROT:P50282; GB:U24441; NID:gll173505; PIDN:AAA90911.1; PID:gll173505
A;Experimental source: skin wounds
C;Comment: This enzyme belongs to the matrix metalloproteinase family, proteolytic enzyme
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C;Genetics:
A;Gene: gelB
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homolog
C;Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase;
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-708/Product: progelatinase B #status predicted <PRO>
F;25-107/Domain: activation peptide #status predicted <ACT>
F;108-708/Product: gelatinase B #status predicted <MAT>
F;214-389/Region: collagen binding #status predicted
F;231-272/Domain: fibronectin type II repeat homology <2F1>
F;289-330/Domain: fibronectin type II repeat homology <2F2>
F;348-389/Domain: fibronectin type II repeat homology <2F3>
F;514-707/Domain: hemopexin repeat homology <PXN>
F;39_121/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F;403/Active site: Glu #status predicted
F;519-707/Disulfide bonds: #status predicted

Query Match 91.5%; Score 236; DB 2; Length 708;
Best Local Similarity 87.2%; Pred. No. 1.6e-23;
Matches 41; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKQLSLPQTGELDSATLKAMRTPRCGVDPDLGRFTQTFEGDLKWHHN 47
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RESULT 3
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N;Alternate names: EC 3.4.24.35 precursor - rabbit
N;Gelatinase B (EC 3.4.24.35)
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A53796; A55398
J.R.Tezuka, K.; Nemoto, K.; Tezuka, Y.; Sato, T.; Ikeda, Y.; Kobori, M.; Kawashima, H.; Egi
R.J.Biol. Chem. 269, 15006-15009, 1994
A;Title: Identification of matrix metalloproteinase 9 in rabbit osteoclasts.
A;Reference number: A53796; MUID:94253056; PMID:8195136
A;Accession: A53796
A;Molecule type: mRNA
A;Residues: 1-707 <TEZ>
A;Cross-references: UNIPROT:P41246; GB:D26514; NID:g499372; PIDN:BAA05520.1; PID:g499373
A;Experimental source: osteoclasts
R;Finl M.E.; Bartlett, J.D.; Matsubara, M.; Rinehart, W.B.; Mody, M.K.; Girard, M.T.; Re
J. Biol. Chem. 269, 28620-28628, 1994
A;Title: The rabbit gene for 92-kDa matrix metalloproteinase. Role of API and AP2 in cel
A;Reference number: A55398; MUID:95050662; PMID:7961810
A;Accession: A55398
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-75, 'P', '77-99', 'ASR', 103-171 <FIN>
A;Cross-references: GB:L36050; NID:g535714; PIDN:AAA64358.1; PID:g535715
C;Genetics:
A;Introns: 46/3; 124/2
C;Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homolog
C;Keywords: glycoprotein; hydrolase; metalloproteinase; zinc; zymogen
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F;20-106/Domain: activation peptide #status predicted <PRO>
F;107-707/Product: 91k neutrophil gelatinase B #status predicted <MAT>
F;230-271/Domain: fibronectin type II repeat homology <2F9>
F;288-329/Domain: fibronectin type II repeat homology <2F8>
F;347-388/Domain: fibronectin type II repeat homology <2F1>
F;510-704/Domain: hemopexin repeat homology <PXN>
F;88,120,127/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status I
F;401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F;402/Active site: Glu #status predicted

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 2.2e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 4
S62307
Gelatinase B (EC 3.4.24.35) precursor - rat
N/Alternate names: collagenase type IV
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S62307; S72371
R/Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 382, 285-288, 1996
A/Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinant
A/Reference number: S62307; MUID:96184505; PMID:8605986
A/Accession: S62307
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-708 <XIA>
A/Cross-references: UNIPROT:P50282; EMBL:U36476
R/Feng, L.
submitted to the EMBL Data Library, September 1995
A/Reference number: S72371
A/Accession: S72371
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127, 'S', 129-708 <FEN>
A/Cross-references: EMBL:U36476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784
C/Superfamily: Gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C/Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-107/Domain: propeptide #status predicted <PRO>
F/25-107/Domain: activation peptide #status predicted <ACT>
F/68-217,393-445/Domain: matrix metalloproteinase homology
F/214-389/Region: collagen binding #status predicted
F/231-272/Domain: fibronectin type II repeat homology
F/289-330/Domain: fibronectin type II repeat homology <2F1>
F/348-389/Domain: fibronectin type II repeat homology <2F2>
F/514-707/Domain: hemopexin repeat homology <PXM>
F/100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F/402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F/403/Active site: Glu #status predicted
F/519-707/Disulfide bonds: #status predicted

Query Match 90.3%; Score 233; DB 2; Length 708;
Best Local Similarity 85.1%; Pred. No. 4.2e-23;
Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 121

RESULT 5
I46031
Gelatinase B (EC 3.4.24.35) - bovine
N/Alternate names: matrix metalloproteinase 9 (MMP9)
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: I46031; S43112
R/Baylis, H.A.; Megson, A.; Hall, R.
Mol. Biochem. Parasitol. 69, 211-222, 1995
A/Title: Infection with *Theileria annulata* induces expression of matrix metalloproteinase
A/Reference number: I46031; MUID:95287902; PMID:7770085
A/Accession: I46031
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 2.2e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 74 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 4
S62307
Gelatinase B (EC 3.4.24.35) precursor - rat
N/Alternate names: collagenase type IV
C/Species: Rattus norvegicus (Norway rat)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S62307; S72371
R/Xia, Y.; Garcia, G.; Chen, S.; Wilson, C.B.; Feng, L.
FEBS Lett. 382, 285-288, 1996
A/Title: Cloning of rat 92-kDa type IV collagenase and expression of an active recombinant
A/Reference number: S62307; MUID:96184505; PMID:8605986
A/Accession: S62307
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-708 <XIA>
A/Cross-references: UNIPROT:P50282; EMBL:U36476
R/Feng, L.
submitted to the EMBL Data Library, September 1995
A/Reference number: S72371
A/Accession: S72371
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-127, 'S', 129-708 <FEN>
A/Cross-references: EMBL:U36476; NID:g1022783; PIDN:AAB01721.1; PID:g1022784
C/Superfamily: Gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C/Keywords: extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-107/Domain: propeptide #status predicted <PRO>
F/25-107/Domain: activation peptide #status predicted <ACT>
F/68-217,393-445/Domain: matrix metalloproteinase homology
F/214-389/Region: collagen binding #status predicted
F/231-272/Domain: fibronectin type II repeat homology
F/289-330/Domain: fibronectin type II repeat homology <2F1>
F/348-389/Domain: fibronectin type II repeat homology <2F2>
F/514-707/Domain: hemopexin repeat homology <PXM>
F/100,402,406,412/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F/402,406,412/Binding site: zinc, catalytic (His) (active) #status predicted
F/403/Active site: Glu #status predicted
F/519-707/Disulfide bonds: #status predicted

Query Match 90.3%; Score 233; DB 2; Length 708;
Best Local Similarity 85.1%; Pred. No. 4.2e-23;
Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 121

RESULT 5
I46031
Gelatinase B (EC 3.4.24.35) - bovine
N/Alternate names: matrix metalloproteinase 9 (MMP9)
C/Species: Bos primigenius taurus (cattle)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: I46031; S43112
R/Baylis, H.A.; Megson, A.; Hall, R.
Mol. Biochem. Parasitol. 69, 211-222, 1995
A/Title: Infection with *Theileria annulata* induces expression of matrix metalloproteinase
A/Reference number: I46031; MUID:95287902; PMID:7770085
A/Accession: I46031
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA

A/Residues: 1-712 <BAY>
A/Cross-references: UNIPROT:P52176; EMBL:X78324; NID:g467620; PIDN:CAA55127.1; PID:g4676.
A/Note: submitted to the EMBL Data Library, March 1994
C/Genetics:
A/Gene: mmp9
C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F/67-216,392-444/Domain: matrix metalloproteinase homology #status atypical <MMP>
F/230-271/Domain: fibronectin type II repeat homology <2F1>
F/288-329/Domain: fibronectin type II repeat homology <2F2>
F/347-388/Domain: fibronectin type II repeat homology <2F3>
F/515-709/Domain: hemopexin repeat homology <PXM>
F/99,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F/401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F/402/Active site: Glu #status predicted

Query Match 87.6%; Score 226; DB 1; Length 712;
Best Local Similarity 84.8%; Pred. No. 3.7e-22;
Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 QKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 QRLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 6
I52580
gelatinase B (EC 3.4.24.35) precursor - mouse
N/Alternate names: collagenase type IV
C/Species: Mus sp. (mouse)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C/Accession: I52580
R/Graubert, T.; Johnston, J.; Berliner, N.
Blood 82, 3192-3197, 1993
A/Title: Cloning and expression of the cDNA encoding mouse neutrophil gelatinase: demonstration of a novel proteinase
A/Reference number: I52580; MUID:9403534; PMID:8219207
A/Accession: I52580
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-730 <RES>
A/Cross-references: GB:S67830; NID:g460863; PIDN:AAB28942.1; PID:g460864
C/Superfamily: gelatinase A; fibronectin type II repeat homology; hemopexin repeat homology
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F/230-271/Domain: fibronectin type II repeat homology <2F1>
F/288-329/Domain: fibronectin type II repeat homology <2F2>
F/347-388/Domain: fibronectin type II repeat homology <2F3>
F/529-729/Domain: hemopexin repeat homology <PXM>
F/100,401,405,411/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F/401,405,411/Binding site: zinc, catalytic (His) (active) #status predicted
F/402/Active site: Glu #status predicted

Query Match 82.8%; Score 213.5; DB 1; Length 730;
Best Local Similarity 85.1%; Pred. No. 1.8e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 47
DB 75 LQKLSLPETGELDSATLKAMRTPRCGVDPDLGRFQTPEGDLKWHHN 120

RESULT 7
JCI456
Gelatinase B (EC 3.4.24.35) precursor - mouse
N/Alternate names: 92K gelatinase; 92K type IV collagenase; matrix metalloproteinase 9 (MMP9)
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: JCI456; S39525; I48296; S38654
R/Tanaka, H.; Hojo, K.; Yoshida, H.; Yoshika, T.; Sugita, K.
Biochem. Biophys. Res. Commun. 190, 732-740, 1993
A/Title: Molecular cloning and expression of the mouse 105-kDa gelatinase cDNA.
A/Reference number: JCI456; MUID:93176173; PMID:8382489
A/Accession: JCI456
A/Molecule type: mRNA

Qy 1 LQQLSLPETGELDSATLKAMRTPRCGVFDLGRFQTFEGDLKW 43

Q. I have a question about the 1992-1993 season. I was told that the 1992-1993 season was the best season for the fishery in many years. Is that correct?

Qy 1 LQQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTPEGDLKWHHNN 47

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 82.25 seconds
(without alignments)
292.617 Million cell updates/sec

Title: US-10-032-376A-8

Perfect score: 258

Sequence: 1 LQQLSLPETGELDSATLKA.....VPLGRFQTPEGLKWHHNN 47

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	258	100.0	707	1	MM09 HUMAN	P14780 homo sapien
2	235	91.1	707	1	MM09 RABIT	P14246 oryctolagus
3	233	90.3	708	1	MM09 RAT	P50282 rattus norv
4	226	87.6	324	2	Q9N282	Q9N282 bos taurus
5	226	87.6	712	1	MM09 BOVIN	P52176 bos taurus
6	216	83.7	149	2	Q9TVB4	Q9TVB4 canis fami
7	216	83.7	704	1	MM09 CANFA	O18733 canis fami
8	213.5	82.8	730	1	MM09 MOUSE	P41245 mus musculu
9	213.5	82.8	730	1	MM09 MOUSE	P41245 mus musculu
10	213.5	82.8	730	2	Q80X18	Q80X18 mus musculu
11	193	74.8	679	2	Q98856	Q98856 cynops pyrr
12	185	71.7	686	2	Q9DE15	Q9DE15 gallus gall
13	177	68.6	673	2	Q90YB3	Q90YB3 paralicthy
14	176	68.2	671	2	Q6PF33	Q6PF33 xenopus lae
15	176	68.2	671	2	Q9W7L6	Q9W7L6 xenopus lae
16	172	66.7	675	2	Q8QFQ6	Q8QFQ6 oncorhynch
17	170	65.9	674	2	Q98TC6	Q98TC6 cyprinus ca
18	168	65.1	690	2	Q9PVM5	Q9PVM5 oryzias lat
19	167	64.7	670	2	Q6DF16	Q6DF16 xenopus tro
20	160	62.0	680	2	Q7T317	Q7T317 brachydanio
21	141	54.7	477	1	MM03 HUMAN	P08254 homo sapien
22	138	53.5	478	1	MM03 RABIT	P28863 oryctolagus
23	135	52.3	145	2	Q9N283	Q9N283 bos taurus
24	134	51.9	475	1	MM03 RAT	P0957 rattus norv
25	133	51.6	139	2	Q9GM68	Q9GM68 sus scrofa
26	133	51.6	476	1	MM10 HUMAN	P09238 homo sapien
27	133	51.6	476	1	MM10 MOUSE	O55123 mus musculu
28	133	51.6	476	1	MM10 RAT	P07152 rattus norv
29	133	51.6	477	1	MM03 MOUSE	P28862 mus musculu
30	133	51.6	479	2	Q922W6	Q922W6 mus musculu
31	131	50.8	478	2	Q6Y4Q5	Q6Y4Q5 canis fami

RESULT 1

ID	MM09 HUMAN	STANDARD;	PRT;	707 AA.
AC	P14780; Q8N725; Q9H4Z1;			
DT	01-APR-1990 (Rel. 14, Created)			
DT	01-APR-1990 (Rel. 14, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	92 kDa type IV collagenase precursor (SC 3.4.24.35) (92 kDa			
DE	gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)			
DE	(GELB).			
GN	Name=MMP9; Synonyms=CLG4B;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 20-37.			
RX	MEDLINE=90008879; PubMed=2551898;			
RA	Wilhelm S.M., Collier I.E., Marmer B.L., Eisen A.Z., Grant G.A.,			
RA	Goldberg G.I.;			
RT	"SV40-transformed human lung fibroblasts secrete a 92-kDa type IV			
RT	collagenase which is identical to that secreted by normal human			
RT	macrophages.";			
RJ	J. Biol. Chem. 264:17213-17221(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91358433; PubMed=1653238;			
RA	Huhtala P., Tuuttila A., Chow L.T., Lohi J., Keski-Oja J.,			
RA	Tryggvason K.;			
RT	"Complete structure of the human gene for 92-kDa type IV collagenase.			
RT	Divergent regulation of expression for the 92- and 72-kilodalton			
RT	enzyme genes in HT-1080 cells.";			
RL	J. Biol. Chem. 266:16485-16490(1991).			
RN	[3]			
RP	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RA	Rieder M.J., Armet T.Z., Carrington D.P., Ozuna M., Kuldanek S.A.,			
RA	Rajkumar N.R., Toth E.J., Yi Q., Nickerson D.A.;			
RT	"SeattlesNPs, NHLBI HL66682 program for genomic applications, UW-			
RT	PHRC, Seattle, WA (URL: http://pga.gs.washington.edu)";			
RL	Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A., AND VARIANT GLN-279.			
RX	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;			
RA	Deloukas P., Matthews L.H., Ashurst J.L., Babbage A.K., Baggeley C.L.,			
RA	Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baggeley C.L.,			
RA	Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,			
RA	Coulson A., Corvillie G.J., Deadman R., Dhani P.D., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			

Q7zwd0 brachydanio
Q70138 mus musculu
Q8c209 mus musculu
Q8c230 mus musculu
Q88766 rattus norv
Q71959 brachydanio
Q8mi18 felis silve
Q9ucj9 homo sapien
Q6dg10 brachydanio
Q7azms brachydanio
Q7c0k9 ambystoma m
Q5pww3 xenopus lae
Q7zt19 xenopus lae
Q9ptu7 oryzias lat

ALIGNMENTS

RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Levesiaho M.H., Leversha M.A., Lloyd D.M., Lovell J.D.,
 RA Marsh V.D., Martin S.L., McConnachie L.J., McIlroy K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
 RA Stuce C.D., Smith M.L., Soderlund C., Stewart C.A., Sulston J.E.,
 RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.,
 RT "The DNA sequence and comparative analysis of human chromosome 20."
 RL Nature 414:865-871 (2001).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Kaha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [6]
 RP SEQUENCE OF 1-11 FROM N.A.
 RX MEDLINE=93149601; PubMed=8426746;
 RA Sato H., Seiki M.,
 RT "Regulatory mechanism of 92 kDa type IV collagenase gene expression
 RT which is associated with invasiveness of tumor cells."
 RL Oncogene 8:395-405 (1993).
 RN [7]
 RP SEQUENCE OF 20-37.
 RX MEDLINE=91355647; PubMed=1653055; DOI=10.1016/1043-4666(91)90021-5;
 RA van Ranst M., Norga K., Masure S., Proost P., Vandekerckhove F.,
 RA Auwerx J., van Damme J., Opdenakker G.,
 RT "The cytokine-protease connection: identification of a 96-kD THP-1
 RT gelatinase and regulation by interleukin-1 and cytokine inducers."
 RL Cytokine 3:231-239 (1991).
 RN [8]
 RP SEQUENCE OF 28-60.
 RC TISSUE=Neutrophils;
 RX MEDLINE=91249834; PubMed=1645657;
 RA Masure S., Proost P., van Damme J., Opdenakker G.,
 RT "Purification and identification of 91-kDa neutrophil gelatinase.
 RT Release by the activating peptide interleukin-8."
 RL Eur. J. Biochem. 198:391-398 (1991).
 RN [9]
 RP CHARACTERIZATION.
 RA Kang K., Lee D.-H.,
 RT "Purification and characterization of human 92-kDa type IV collagenase
 RT (gelatinase B)."
 RL Exp. Mol. Med. 28:161-165 (1996).
 RN [10]
 RP 3D-STRUCTURE MODELING.
 RA Mallena S.C., Sagajkar R.D.,
 RT "Theoretical model of human type IV collagenase precursor."

RL Submitted (APR-2002) to the PDB data bank.
 RN [11]
 RP VARIANTS VAL-20; LYS-82 AND GLN-279.
 RX MEDLINE=20065865; PubMed=10598006;
 RA Zhang B., Henney A., Eriksson P., Hamsten A., Watkins H., Ye S.,
 RT "Genetic variation at the matrix metalloproteinase-9 locus on
 RT chromosome 20q12.2-13.1";
 RL Hum. Genet. 105:418-423 (1999).
 CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- SUBUNIT: Exists as monomer, disulfide-linked homodimer, and as a
 CC heterodimer with a 25 kDa protein. Macrophages and transformed
 CC cell lines produce only the monomeric form.
 CC -1- TISSUE SPECIFICITY: Produced by normal alveolar macrophages and
 CC granulocytes.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 DR EMBL: J05070; AAA51539.1; -;
 DR EMBL: D10051; BAA20967.1; -;
 DR EMBL: AF538844; AM97934.1; -;
 DR EMBL: AL162458; CAC10459.1; -;
 DR EMBL: BC006093; AAH06093.1; -;
 DR PIR: A34458; A34458.
 DR PDB: 1GKC; X-ray; A/B=106-443.
 DR PDB: 1GKD; X-ray; A/B=106-443.
 DR PDB: 1ITV; X-ray; A/B=513-707.
 DR PDB: 1L6J; X-ray; A=20-444.
 DR PDB: 1LKG; Model; A=1-707.
 DR MEROPS: M10.004; -;
 DR GlycoSuiteDB; P14780; -;
 DR Genew; HGNC:7176; MMP9.
 DR H-InvDB; HIX0015874; -;
 DR MIM; 120361; -;
 DR GO: 0005615; C:extracellular space; TAS.
 DR GO: 0008133; F:collagenase activity; TAS.
 DR GO: 0008270; F:zinc ion binding; TAS.
 DR GO: 0006508; P:proteolysis and peptidolysis; TAS.
 DR InterPro: IPR000562; FN_Type_II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR009070; PGSD_like.
 DR InterPro: IPR006970; PT.
 DR Pfam: PF00040; fn2; 3.
 DR Pfam: PF00045; Hemopexin; 4.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRXIN.
 DR ProDom; PD000995; FN_Type_II; 2.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 3.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Calcium; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19
 FT PROPEP 20 106 Activation peptide.

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FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronectin type-II 1.

Query Match 100.0%; Score 258; DB 1; Length 707;
Best Local Similarity 100.0%; Pred. No. 3.8e-26; Indels 0; Gaps 0;
Matches 47; Conservative 0; Mismatches 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCVDPDLGRFQTPEGDLKWHHN 47
    |||||
Db 74 LQKLSLPETGELDSATLKAMRTPRCVDPDLGRFQTPEGDLKWHHN 120

RESULT 2
MM09 RABIT STANDARD; PRT; 707 AA.
AC P4126;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=MMP9;
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Japanese white; TISSUE=Bone;
RA MEDLINE=94253056; PubMed=819136;
RA Tezuka K.I., Nemoto K., Tezuka Y., Sato T., Ikeda Y., Kobori M.,
RA Kawashima H., Eguchi H., Hakeda Y., Kumegawa M.;
RT "Identification of matrix metalloproteinase 9 in rabbit osteoclasts.";
RL J. Biol. Chem. 269:15006-15009(1994).
RL [2]
RN SEQUENCE OF 1-171 FROM N.A.
RP STRAIN=New Zealand white; TISSUE=Liver;
RX MEDLINE=95050662; PubMed=7961810;
RA Fini M.E., Bartlett J.D., Mateubara M., Rinehart W.B., Mody M.K.,
RA Girard M.T., Rainville M.;
RT "The rabbit gene for 92-kDa matrix metalloproteinase. Role of AP1 and
RT AP2 in cell type-specific transcription.";
RL J. Biol. Chem. 269:28620-28628(1994).
CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
CC types IV and V.
CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -1- TISSUE SPECIFICITY: Osteoclasts.
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; D26514; BAA05520.1; -
CC EMBL; L36050; AAA64358.1; -
CC PIR; A53796; A53796.
CC HSP; P14780; IGKC.
CC MEROPS; M10.004; -.
CC InterPro; IPR000562; FN Type II.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M2n_BS.
CC InterPro; IPR008026; Peptidase_M.
CC InterPro; IPR009070; PGSD_like.
CC InterPro; IPR006970; PT.

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DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF01933; Peptidase_M10_N; 1.
DR Pfam; PF04886; PT; 1.
DR PRINTS; PR00013; FNTYPEII.
DR PRINTS; PR00138; MATRIKIN.
DR PRODOM; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; FN; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
FT SIGNAL 1 19
FT PROPEP 20 106 Activation peptide (By similarity).
FT CHAIN 107 707 92 kDa type IV collagenase.
FT DOMAIN 223 280 Fibronectin type-II 1.
FT DOMAIN 281 339 Fibronectin type-II 2.
FT DOMAIN 340 397 Fibronectin type-II 3.
FT DOMAIN 513 707 Hemopexin-like.
FT SITE 99 99 Cysteine switch (By similarity).
FT METAL 401 401 Zinc (catalytic) (By similarity).
FT ACT_SITE 402 402 Zinc (catalytic).
FT METAL 405 405 Zinc (catalytic) (By similarity).
FT METAL 411 411 Zinc (catalytic) (By similarity).
FT CARBOHYD 88 88 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
FT DISULFID 516 704 By similarity.
FT CONFLICT 76 76 K -> P (in Ref. 2).
FT CONFLICT 100 102 GVP -> ASR (in Ref. 2).
SQ SEQUENCE 707 AA; 78307 MW; 053BCE8DC4D4758F CRC64;

Query Match 91.1%; Score 235; DB 1; Length 707;
Best Local Similarity 87.2%; Pred. No. 5.1e-23;
Matches 41; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LQKLSLPETGELDSATLKAMRTPRCVDPDLGRFQTPEGDLKWHHN 47
    |||||
Db 74 LQKLSLPETGELDSATLKAMRTPRCVDPDLGRFQTPEGDLKWHHN 120

RESULT 3
MM09 RAT STANDARD; PRT; 708 AA.
AC P50282;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
DE (GELB).
GN Name=Mmp9;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Fischer 344;
RX MEDLINE=96184505; PubMed=8605986; DOI=10.1016/0014-5793(96)00185-8;
RA Xia Y., Garcia G., Chen S., Wilson C.B., Peng L.;
RT "Cloning of rat 92-kDa type IV collagenase and expression of an active
RT recombinant catalytic domain.";
RL FEBS Lett. 382:285-288(1996).
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RX MEDLINE=96069602; PubMed=7590350; DOI=10.1016/0378-1119(95)00447-E;

```

Okada A., Santavica M., Basset P.;
 "The cDNA cloning and expression of the gene encoding rat gelatinase
 B.";
 Gene 164:317-321(1995).
 CC -!- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -!- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 types IV and V.
 CC -!- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U36476; AAB01721.1; -;
 DR EMBL; U24441; AAA90911.1; -;
 DR PIR; JC4364; JC4364.
 DR PIR; S62907; S62907.
 DR HSP; P14780; LGKC.
 DR MEROPS; M10.004; -;
 DR RGD; 621320; Mmp9.
 DR InterPro; IPR000562; FN_Type_II; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR006970; PT.
 DR Pfam; PF00040; fn2; 3.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR Pfam; PF04886; PT; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 2.
 DR SMART; SM00059; FN2; 3.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 2.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolyase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 19 By similarity.
 FT PROPEP 20 107 Activation peptide (By similarity).
 FT CHAIN 108 708 92 kDa type IV collagenase.
 FT DOMAIN 224 281 Fibronectin type-II 1.
 FT DOMAIN 282 340 Fibronectin type-II 2.
 FT DOMAIN 341 398 Fibronectin type-II 3.
 FT DOMAIN 516 708 Hemopexin-like.
 FT SITE 100 100 Cysteine switch (By similarity).
 FT METAL 402 402 Zinc (catalytic) (By similarity).
 FT ACT_SITE 403 403 Zinc (catalytic) (By similarity).
 FT METAL 406 406 Zinc (catalytic) (By similarity).
 FT METAL 412 412 Zinc (catalytic) (By similarity).
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).
 FT DISULFID 121 121 By similarity.
 FT CONFLICT 519 707 S -> N (in Ref. 2).
 FT CONFLICT 112 112 D -> E (in Ref. 2).
 FT CONFLICT 326 327 AD -> LY (in Ref. 2).
 FT CONFLICT 364 364 S -> G (in Ref. 2).
 FT CONFLICT 441 441 H -> Q (in Ref. 2).
 FT CONFLICT 472 472 S -> P (in Ref. 2).
 FT CONFLICT 515 515 D -> V (in Ref. 2).
 FT CONFLICT 551 551 N -> S (in Ref. 2).

FT CONFLICT 566 566 F -> L (in Ref. 2).
 FT CONFLICT 568 568 S -> A (in Ref. 2).
 FT CONFLICT 579 579 P -> S (in Ref. 2).
 FT CONFLICT 586 589 LMAQ -> SGRK (in Ref. 2).
 FT CONFLICT 597 597 S -> T (in Ref. 2).
 FT CONFLICT 669 669 Q -> H (in Ref. 2).
 SQ SEQUENCE 708 AA; 78610 MW; D57DC0D1B93A778C CRC64;
 Query Match 90.3%; Score 233; DB 1; Length 708;
 Best Local Similarity 85.1%; Pred. No. 9.6e-23;
 Matches 40; Conservative 6; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LKQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 Db 75 LKQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 121
 RESULT 4
 Q9N282 PRELIMINARY; PRT; 324 AA.
 AC Q9N282;
 DT 01-OCT-2000 (TREMELrel. 15, Created)
 DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE MMP-9 (Fragment).
 GN Name-bmmp-9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sato T., Hirata M., Ito A., Hashizume K.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB043996; BAA96389.1; -;
 DR HSP; P14780; LGKD.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR000562; FN_Type_II.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR009070; PGSD_like.
 DR Pfam; PF00040; fn2; 2.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00013; FNTYPEII.
 DR PRINTS; PR00138; MATRIXIN.
 DR PRODOM; PD000995; FN_Type_II; 2.
 DR SMART; SM00059; FN2; 2.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00023; FIBRONECTIN_2; 1.
 FT NON_TER 324 324
 SQ SEQUENCE 324 AA; 36273 MW; 4137C9820C28B080 CRC64;
 Query Match 87.6%; Score 226; DB 2; Length 324;
 Best Local Similarity 84.8%; Pred. No. 3.5e-22;
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 2 QKQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 47
 Db 75 QKQLSLPETGELDSATLKAMRTPCGVDPDLGRFQTFEGDLKWHHN 120
 RESULT 5
 MM09 BOVIN STANDARD; PRT; 712 AA.
 ID MM09 BOVIN
 AC P52176;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa

DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN Name=MMP9;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Leukocyte;
 RX MEDLINE=95287902; PubMed=7770085; DOI=10.1016/0166-6851(94)00216-A;
 RA Baylis H.A., Megson A., Hall R.;
 RT "Infection with Theileria annulata induces expression of matrix
 RT metalloproteinase 9 and transcription factor AP-1 in bovine
 RT leucocytes.";
 RL Mol. Biochem. Parasitol. 69:211-222(1995).
 CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
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 CC -----
 DR EMBL: X78324; CA55127.1; --
 DR PIR: I46031; I46031.
 DR HSP: P14780; IGD.
 DR MEROPS: M10.004; --
 DR InterPro: IPR000562; FN Type II.
 DR InterPro: IPR000585; Hemopexin.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR006025; Pept_M_Zn_BS.
 DR InterPro: IPR006026; Peptidase_M.
 DR InterPro: IPR009070; PGBD_like.
 DR InterPro: IPR006970; PT.
 DR Pfam: PF00040; fn2; 3.
 DR Pfam: PF00045; Hemopexin; 4.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR Pfam: PF04886; PT; 1.
 DR PRINTS: PR00013; FNTYPEII.
 DR PRINTS: PR00138; MATRPIXIN.
 DR ProDom: PD000995; FN_Type_II; 2.
 DR SMART: SM00059; FN2; 3.
 DR SMART: SM00120; HX; 4.
 DR SMART: SM00235; ZnMc; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE: PS00023; FIBRONECTIN_2; 3.
 DR PROSITE: PS00024; HEMOPEXIN; FALSE_NEG.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 19
 FT CHAIN 20 106 Activation peptide.
 FT CHAIN 107 712 92 kDa type IV collagenase.
 FT DOMAIN 223 280 Fibronectin type-II 1.
 FT DOMAIN 281 339 Fibronectin type-II 2.
 FT DOMAIN 340 397 Fibronectin type-II 3.
 FT DOMAIN 518 712 Hemopexin-like.
 FT SITE 99 99 Cysteine switch (By similarity).
 FT METAL 401 401 Zinc (catalytic) (By similarity).
 FT ACT_SITE 402 402 By similarity.
 FT METAL 405 405 Zinc (catalytic) (By similarity).
 FT METAL 411 411 Zinc (catalytic) (By similarity).

FT DISULFID 521 709 By similarity.
 FT CARBOHYD 38 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 712 AA; 79087 MW; E7FDA28372AEEOCE CRC64;
 Query Match 87.6%; Score 226; DB 1; Length 712;
 Best Local Similarity 84.8%; Pred. No. 8.7e-22;
 Matches 39; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 QKQLSLPETGELDSATLKAMRTPCRGVDPDLGRFQTFEGDLKWHHN 47
 Db 75 QRRSLPETGELDSTTLNAMPAPRCGVDPDVGRTFEGELKWHHN 120
 RESULT 6
 Q9TVB4
 ID Q9TVB4 PRELIMINARY; PRT; 149 AA.
 AC Q9TVB4;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Type IV collagenase MMP-9 (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fibrosarcoma;
 RA Paria B.C., Kitchell B.E.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF147104; AAD31323.1; --
 DR HSP: P14780; IGD.
 DR GO: GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO: GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO: GO:0006508; F:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR001818; Pept_M10A_M12B.
 DR InterPro: IPR009070; PGBD_like.
 DR Pfam: PF00413; Peptidase_M10; 1.
 DR Pfam: PF03933; Peptidase_M10_N; 1.
 DR PRINTS: PR00138; MATRPIXIN.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; 1.
 DR NON_TER 149 149
 SQ SEQUENCE 149 AA; 17025 MW; CA6A5062EFDCCBBF CRC64;
 Query Match 83.7%; Score 216; DB 2; Length 149;
 Best Local Similarity 78.7%; Pred. No. 3.2e-21;
 Matches 37; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LQKQLSLPETGELDSATLKAMRTPCRGVDPDLGRFQTFEGDLKWHHN 47
 Db 74 LQRRALPETGELDKTTLEARNAPRCGVDPDLGRFQTFEGDLKWHND 120
 RESULT 7
 MM09 CANFA
 ID MM09 CANFA STANDARD; PRT; 704 AA.
 AC O18733; O19130;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB).
 GN Name=MMP9;
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.

DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE 92 kDa type IV collagenase precursor (EC 3.4.24.35) (92 kDa
 DE gelatinase) (Matrix metalloproteinase-9) (MMP-9) (Gelatinase B)
 DE (GELB)
 GN Names=Mmp9; Synonyms=C194b;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Bone;
 RX MEDLINE=941179406; PubMed=8132709; DOI=10.1083/jcb.124.6.1091;
 RA Reponen P., Sahlberg C., Munaut C., Theleff I., Tryggvason K.;
 RT "High expression of 92-kD type IV collagenase (gelatinase B) in the
 RT osteoclast lineage during mouse development.";
 RL J. Cell Biol. 124:1091-1102(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=931176173; PubMed=8382489;
 RA Tanaka H., Hojo K., Yoshida H., Yoshioka T., Sugita K.;
 RT "Molecular cloning and expression of the mouse 105-kDa gelatinase
 RT cDNA.";
 RL Biochem. Biophys. Res. Commun. 190:732-740(1993).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Liver;
 RX MEDLINE=94062823; PubMed=8243459;
 RA Masure S., Nys G., Fiten P., van Damme J., Opdenakker G.;
 RT "Mouse gelatinase B. cDNA cloning, regulation of expression and
 RT glycosylation in WEHI-3 macrophages and gene organisation.";
 RL Eur. J. Biochem. 218:129-141(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94033534; PubMed=8219207;
 RA Graubert T., Johnston J., Berliner N.;
 RT "Cloning and expression of the cDNA encoding mouse neutrophil
 RT gelatinase: demonstration of coordinate secondary granule protein gene
 RT expression during terminal neutrophil maturation.";
 RL Blood 82:3192-3197(1993).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Lung;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
 RA Nikaido I., Osato N., Sato R., Suzuki H., Yamana I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
 RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
 RA Gaasterland T., Gariboldi M., Glessi C., Godzik A., Gough J.,
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sadelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tonita M.,
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hahizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).
 CC -1- FUNCTION: Could play a role in bone osteoclastic resorption.
 CC -1- CATALYTIC ACTIVITY: Cleavage of gelatin types I and V and collagen
 CC types IV and V.
 CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 3 fibronectin type II domains.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL; Z27231; CAA81745.1; -;
 CC EMBL; D12712; BAA02208.1; -;
 CC EMBL; X72794; CAA51314.1; -;
 CC EMBL; X72795; CAA51315.1; -;
 CC EMBL; S67830; AAB28942.1; -;
 CC EMBL; AK004651; BAB23442.1; -;
 CC PIR; JCI456; JCI456.
 CC HSSP; P14780; 1GKC.
 CC MEROPS; M10.004; -;
 CC MGD; MG1:97011; Mmp9.
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 CC InterPro; IPR000585; Hemopexin.
 CC InterPro; IPR001818; Pept_M10A_M12B.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 CC InterPro; IPR006026; Peptidase_M.
 CC InterPro; IPR009070; PGBD_like.
 CC InterPro; IPR006970; PT.
 CC Pfam; PF00040; fn2; 3.
 CC Pfam; PF00045; Hemopexin; 4.
 CC Pfam; PF00413; Peptidase_M10; 1.
 CC Pfam; PF03933; Peptidase_M10_N; 1.
 CC Pfam; PF04886; PT; 2.
 CC PRINTS; PR00013; ENTPEP11.
 CC PRINTS; PR00138; MATR1XIN.
 CC ProDom; PD000995; FN_Type_II; 2.
 CC SMART; SM00059; FN2; 3.
 CC SMART; SM00120; HX; 4.
 CC SMART; SM00235; ZnMc; 1.
 CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 CC PROSITE; PS00023; FIBRONECTIN_2; 3.
 CC PROSITE; PS00024; HEMOPEXIN; 1.
 CC PROSITE; PS00142; ZINC_PROTEASE; 1.
 CC Calcium; Collagen degradation; Extracellular matrix; Glycoprotein;
 CC Hydrolase; Metalloprotease; Polymorphism; Repeat; Signal; Zinc;
 CC Zymogen.
 KW SIGNAL 1 19 By similarity.
 FT PROPEP 20 107 Activation peptide (By similarity).
 FT CHAIN 108 730 92 kDa type IV collagenase.
 FT DOMAIN 223 280 Fibronectin type-II 1.
 FT DOMAIN 281 339 Fibronectin type-II 2.
 FT DOMAIN 340 397 Fibronectin type-II 3.
 FT DOMAIN 531 730 Hemopexin-like.
 FT SITE 100 100 Cysteine switch (By similarity).
 FT METAL 401 401 Zinc (catalytic) (By similarity).
 FT ACT_SITE 402 402 Zinc (catalytic).
 FT METAL 411 411 Zinc (catalytic) (By similarity).
 FT METAL 411 411 Zinc (catalytic) (By similarity).
 FT CARBOHYD 39 39 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 FT DISULFID 534 729 By similarity.
 FT VARIANT 514 519 A -> P.
 FT VARIANT 639 639 P -> L.
 FT VARIANT 711 711 P -> H.
 FT VARIANT 20 20 A -> C (in Ref. 4).
 FT CONFLICT 25 26 QP -> HA (in Ref. 4).
 FT CONFLICT 25 26


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FT CONFLICT 466 466 P -> T (in Ref. 5).
FT CONFLICT 514 514 A -> P (in Ref. 5).
FT CONFLICT 639 639 P -> L (in Ref. 5).
FT CONFLICT 711 711 P -> H (in Ref. 5).
SQ SEQUENCE 730 AA; 80453 MW; E1911F6D5CCAC059 CRC64;

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Best Local Similarity 85.1%; Pred.No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 LQKQLSLPQTGELDSOTLKAIKRTPRCGVPDVGFRFQTFKG-LKWDHEN 120

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DT 01-JUN-2003 (T-EMBLrel. 24, Created)
DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase 9.
GN Name=Mmp9;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Olfactory epithelium;
RA Srausberg R.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC046991; AAH46991.1; -.
DR HSSP; P14780; 1GKC.
DR MGD; MG1:97011; Mmp9.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004222; F:metalloendopeptidase activity; IDA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR InterPro; IPR006970; PT.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
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Db 75 LQKQLSLPQTGELDSOTLKAIKRTPRCGVPDVGFRFQTFKG-LKWDHEN 120

Query Match 82.8%; Score 213.5; DB 2; Length 730;
Best Local Similarity 85.1%; Pred.No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

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RESULT 11
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ID Q98856
AC Q98856;
DT 01-FEB-1997 (T-EMBLrel. 02, Created)
DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Gelatinase-b.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
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RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=96270627; PubMed=8692902; DOI=10.1073/pnas.93.13.6819;
RA Miyazaki K., Uchiyama K., Imokawa Y., Yoshizato K.;
RT "Cloning and characterization of cDNAs for matrix metalloproteinases
RT of regenerating newt limbs.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:6819-6824(1996).
DR EMBL; D82052; BAAL1523.1; -.
DR HSSP; P08253; 1J7M.
DR MEROPS; M10.004; -.
DR GO; GO:000578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0004508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000562; FN_Type_II.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
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DR PRINTS; PR00138; MATRILIN.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
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DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN_1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
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Best Local Similarity 85.1%; Pred.No. 4.5e-20;
Matches 40; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 LQKQLSLPETGELDSATLKAMRTPRCGVPDLGRFQTFEGDLKWHHN 47
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Matches 33; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

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DR HSPS; F33435; ICXV.
DR MEROPS; M10_004; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPRO000563; FN_Type_II.
DR InterPro; IPRO000585; Hemopexin.
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DR InterPro; IPRO060025; Pept_M_Zn_BS.
DR InterPro; IPRO09070; PGBD_like.
DR Pfam; PF00040; fn2; 3.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00013; FNTPPEII.
DR PRINTS; PR00138; MATRIXIN.
DR ProDom; PD000995; FN_Type_II; 2.
DR SMART; SM00059; FN2; 3.
DR SMART; SM00120; HK; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00023; FIBRONECTIN_2; 3.
DR PROSITE; PS00024; HEMOPEXIN; UNKNOWN 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN 1.
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 26.3077 Seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pdp.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pdp.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pdp.*
- 5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pdp.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pdp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	292	100.0	469	3	US-08-448-489-12
3	292	100.0	469	3	US-09-521-220-16
4	292	100.0	469	3	US-09-391-104-23
5	292	100.0	469	4	US-09-949-016-6223
6	292	100.0	469	4	US-09-689-730-12
7	292	100.0	431	4	US-09-949-016-10875
8	214	73.3	444	1	US-09-178-002-2
9	214	73.3	466	3	US-08-704-711A-17
10	214	73.3	466	3	US-09-521-220-17
11	214	73.3	467	1	US-09-178-002-4
12	214	73.3	467	3	US-09-391-104-24
13	214	73.3	468	3	US-08-448-489-13
14	214	73.3	468	4	US-09-689-730-13
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17	189	64.7	476	3	US-09-521-220-21
18	189	64.7	476	3	US-09-391-104-22
19	189	64.7	476	4	US-09-949-016-6224
20	189	64.7	476	4	US-09-689-730-14
21	189	64.7	477	3	US-08-704-711A-20
22	189	64.7	477	3	US-08-448-489-15
23	189	64.7	477	3	US-08-281-313-1
24	189	64.7	477	3	US-09-521-220-20
25	189	64.7	477	3	US-09-391-104-21
26	189	64.7	477	4	US-09-689-730-15
27	189	64.7	484	4	US-09-949-016-10877

28	163	55.8	471	3	US-09-391-104-25	Sequence 25, Appl
29	163	55.8	480	4	US-09-949-016-10560	Sequence 10560, A
30	163	55.8	513	4	US-09-862-631-4	Sequence 4, Appl
31	159	54.5	470	3	US-08-068-392-2	Sequence 2, Appl
32	159	54.5	470	3	US-08-396-988-2	Sequence 2, Appl
33	159	54.5	470	3	US-09-391-104-26	Sequence 26, Appl
34	159	54.5	473	4	US-09-949-016-10876	Sequence 10876, A
35	158	54.1	663	4	US-09-194-468A-30	Sequence 30, Appl
36	154	52.7	471	4	US-08-994-689C-1	Sequence 1, Appl
37	151	51.7	264	3	US-09-009-156-6	Sequence 6, Appl
38	151	51.7	264	3	US-09-372-154-6	Sequence 6, Appl
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40	151	51.7	267	3	US-09-391-104-27	Sequence 27, Appl
41	151	51.7	267	4	US-08-689-730-18	Sequence 18, Appl
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43	151	51.7	277	4	US-09-949-016-8131	Sequence 8131, Ap
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45	147	50.3	471	4	US-08-994-689C-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-08-704-711A-16
; Sequence 16, Application US/08704711a
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horet
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711a
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-704-711A-16

; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6223
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-6223

Query Match 100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 6

US-09-689-730-12
; Sequence 12, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-250P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-12

Query Match 100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 7

US-09-949-016-10875
; Sequence 10875, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 10875
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10875

Query Match 100.0%; Score 292; DB 4; Length 491;
Best Local Similarity 100.0%; Pred. No. 4.3e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
Db 89 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 142

RESULT 8

US-09-178-002-2
; Sequence 2, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-2

Query Match 73.3%; Score 214; DB 1; Length 444;
Best Local Similarity 70.4%; Pred. No. 1.3e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
Db 43 MQEFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRN 96

RESULT 9

US-08-704-711A-17
; Sequence 17, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLYRIEN 119

RESULT 10
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17

Query Match 73.3%; Score 214; DB 3; Length 466;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLYRIEN 119

RESULT 11
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-178-002-4

Query Match 73.3%; Score 214; DB 1; Length 467;
Best Local Similarity 70.4%; Pred. No. 1.4e-20;
Matches 38; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
Db 66 MQRFFGLNVTGKPNBETLDMKKPCGVPDSSGGFMLTPGNPKWERTNLYRIEN 119

RESULT 12
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-391-104-24

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 20.4231 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFFGLKVTGKPDATLVK.....VLTEGNRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	292	100.0	469	1 KCHUI	interstitial colla
2	283	96.9	468	1 KCHUI	interstitial colla
3	270	92.5	469	1 KCPGI	interstitial colla
4	234	80.1	469	1 KCB0I	interstitial colla
5	231.5	79.3	384	2 I51267	collagenase (EC 3.
6	214	73.3	467	1 KCHUN	neutrophil collage
7	189	64.7	476	1 KCHUS2	stromelysin 2 (EC
8	189	64.7	477	1 KCHUS1	stromelysin 1 (EC
9	186	63.7	478	1 KCHRS1	stromelysin 1 (EC
10	173	59.2	476	1 JC6505	stromelysin 2 (EC
11	173	59.2	477	1 KCMRS1	stromelysin 1 (EC
12	172	58.9	475	1 KCMRTH	stromelysin 1 (EC
13	172	58.9	483	2 JC5743	matrix metalloprot
14	168	57.5	472	2 S29243	interstitial colla
15	167	57.2	476	1 KCHRS2	stromelysin 2 (EC
16	163	55.8	471	2 A53711	collagenase 3 (EC
17	162	55.5	466	2 A23685	interstitial colla
18	159	54.5	470	2 A49499	gelatinolastase HM
19	158	54.1	663	1 S46492	gelatinase A (EC 3
20	155	53.1	267	2 A57490	matrilysin (EC 3.4
21	151	51.7	267	1 KCHUM	matrilysin (EC 3.4
22	146	50.0	662	2 S70365	gelatinase A (EC 3
23	144	49.3	462	2 A24201	macrophage elastas
24	144	49.3	660	1 A28153	gelatinase A (EC 3
25	144	49.3	662	2 A42496	gelatinase A (EC 3
26	144	49.3	662	2 S34780	gelatinase A (EC 3
27	135	46.2	708	2 S62907	gelatinase B (EC 3
28	134.5	46.1	582	2 I38028	matrix metalloprot
29	133	45.5	708	2 JC3464	gelatinase B (EC 3

RESULT 1

KCHUI

interstitial collagenase (EC 3.4.24.7) precursor [validated] - human

N/Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col.

C/Species: Homo sapiens (man)

C/Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C/Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S53;

R/Template: N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-Stev

Cancer Res. 50, 5431-5437, 1990

A/Title: Cloning and characterization of human tumor cell interstitial collagenase.

A/Reference number: A37308; MUID:90352587; PMID:2167156

A/Accession: A37308

A/Molecule type: mRNA

A/Residues: 1-469 <TEM>

A/Cross-references: UNIPROT:P03956; GB:X54925; NID:G30125; PIDN:CAA38691.1; PID:G30126

R/Brinckhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.

J. Clin. Invest. 79, 542-546, 1987

A/Title: Molecular cloning of human synovial cell collagenase and selection of a single

A/Reference number: S22766; MUID:87109799; PMID:3027129

A/Accession: S22766

A/Molecule type: DNA

A/Residues: 1-63,65-70 <BRI>

A/Cross-references: EMBL:M15996; NID:G180666; PIDN:AAA35700.1; PID:G180667

R/Angel, P.; Baumann, I.; Stein, B.; Delius, H.; Rahmendorf, H.J.; Herrlich, P.

Mol. Cell. Biol. 7, 2256-2266, 1987

A/Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene

A/Reference number: I57620; MUID:87257941; PMID:3037355

A/Accession: I57620

A/Status: preliminary; translated from GB/EMBL/DDBJ

A/Molecule type: DNA

A/Residues: 1-35 <RES>

A/Cross-references: GB:M16567; NID:G180668; PIDN:AAAS2033.1; PID:G180669

R/Goldberg, G.I.; Wilhelm, S.W.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.

J. Biol. Chem. 261, 6600-6605, 1986

A/Title: Human fibroblast collagenase. Complete primary structure and homology to an onc

A/Reference number: A00996; MUID:86196089; PMID:3009463

A/Accession: A00996

A/Molecule type: mRNA

A/Residues: 1-114, 'R', 116-409, 'S', 411-469 <GOL>

A/Cross-references: GB:M13509; NID:G180664; PIDN:AAA35699.1; PID:G180665

A/Note: part of this sequence was confirmed by protein sequencing of the proenzyme

R/Whitham, S.E.; Murphy, G.; Angel, P.; Rahmendorf, H.J.; Smith, B.J.; Lyons, A.; Harris,

Biochem. J. 240, 913-916, 1986

A/Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis

A/Reference number: A90336; MUID:87156645; PMID:3030290

A/Accession: D29157

A/Molecule type: mRNA

A/Residues: 1-199, 'H', 201-207, 'T', 209-469 <WHI>

A/Cross-references: EMBL:X05231; NID:G38266; PIDN:CAA28858.1; PID:G38267

A/Note: parts of this sequence, including the amino end of the proenzyme and of the matu

R/Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Brown, A.S.; Birkedal-Hansen, H.

Biochemistry 27, 6751-6758, 1988

gelatinase B (EC 3
gelatinase B (EC 3
matrix metalloprot
matrix metalloprot
gelatinase B (EC 3
pro-matrix metallo
gelatinase B (EC 3
gelatinase B (EC 3
matrix metalloprot
probable metallopr
metalloproteinase
probable metallopr
probable metallopr
probable matrix me
hypochemical prote
probable matrix me

707 1 A34458
707 1 A53796
582 2 I84471
669 2 I38029
712 1 I46031
82 2 PW0052
730 1 I52580
730 2 JC1456
582 2 I48673
364 2 E71433
341 2 T51957
342 2 G84885
305 2 T08836
579 2 T37248
598 2 T32166
521 2 T37252

ALIGNMENTS

A;Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzymatic end of the activated enzyme. PMID:2461732
A;Reference number: A44518; MUID:89062403; PMID:2461732
A;Accession: A44518
A;Molecule type: protein
A;Residues: 270-305 <BIR>
R;Clark, I.M.; Cawston, T.E.
Biochem. J. 263, 201-206, 1989
A;Title: Fragments of human fibroblast collagenase. Purification and characterization.
A;Reference number: S06132; MUID:90104231; PMID:2557822
A;Accession: S06132
A;Status: preliminary
A;Molecule type: protein
A;Residues: 100-102,'P',104-107,'XX',110-112;270-277,'X',279-280,'X',282-287 <CLA>
R;Clark, M.W.; Walakowits, L.A.; Shah, T.K.; Vanniddlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta stimulated cells.
A;Reference number: A60964; MUID:91059606; PMID:2173990
A;Accession: B60964
A;Molecule type: protein
A;Residues: 24-35;100-108;270-272,'X',274,'X',276 <LAR>
R;Suzuki, K.; Nagase, H.; Ito, A.; Englund, J.J.; Salvesen, G.
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990
A;Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rheumatoid synovial cells.
A;Reference number: S10595; MUID:90380300; PMID:2169257
A;Accession: S10595
A;Molecule type: protein
A;Residues: 20-102 <SU2>
R;Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.
Biochem. J. 305, 301-306, 1995
A;Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collagenase) and 3 (matrilysin) by tissue inhibitors of metalloproteinases (TIMPs).
A;Reference number: S53438; MUID:95126921; PMID:7826345
A;Accession: S53438
A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-108 <SU2>
R;Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A;Title: Multiple modes of activation of latent human fibroblast collagenase: evidence for a role for tissue inhibitors of metalloproteinases (TIMPs).
A;Reference number: A44517; MUID:90115877; PMID:2153297
A;Contents: annotation; disulfide bond; activation mechanism
R;Salowe, S.P.; Marcy, A.I.; Cuca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes
Biochemistry 31, 4535-4540, 1992
A;Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry of zinc binding and effect of zinc on the catalytic activity.
A;Reference number: A43031; MUID:92256384; PMID:1581308
A;Contents: annotation; zinc ligand in proenzyme
A;Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the catalytic site are activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase can be activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.
C;Genetics:
A;Gene: GDB:MMP1; CUG
A;Cross-references: GDB:119783; OMIM:120353
A;Map position: 11q22.2-11q22.3
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C-supernatant; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-469/Product: procollagenase #status experimental <PRO>
F;20-99/Domain: activation peptide #status experimental <ACT>
F;60-261/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-469/Product: interstitial collagenase #status experimental <MAT>
F;272-466/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;120,143/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;269-270/Cleavage site: Pro-Phe (autolytic) #status experimental
F;278-466/Disulfide bonds: #status experimental

Query Match 100.0%; Score 292; DB 1; Length 469;

Best Local Similarity 100.0%; Pred. No. 2.8e-28;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFGKLVGKPDAAETLKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
Db 67 MQEFGKLVGKPDAAETLKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 120
|||||
RESULT 2
KCRBI
Interstitial collagenase (EC 3.4.24.7) precursor - rabbit
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase; Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A27500; B27500; I46694
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Gross, R.H.; Brinckerhoff, C.E.
Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloproteinases.
A;Reference number: A27500; MUID:88077876; PMID:2825772
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <PIN>
A;Cross-references: UNIPROT:P13943; GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391;399-468 <PI2>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerhoff, C.E.
Coll. Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial cell collagenase and human fibroblast collagenase.
A;Reference number: I46694; MUID:87029174; PMID:3021384
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <PI3>
A;Cross-references: GB:M25663; NID:9531211; PIDN:AAA31203.1; PID:9531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the activation peptide by other proteinases.
C;Comment: Procollagenase can be activated without removal of the activation peptide. Stimulation of the catalytic activity is observed in the presence of the activation peptide.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active.
C;Genetics:
A;Introns: 34/3; 116/2; 166/1; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
A;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C-supernatant; interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-468/Product: procollagenase #status predicted <PRO>
F;19-98/Domain: activation peptide #status predicted <ACT>
F;59-260/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;99-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;119,142/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

Query Match 96.9%; Score 283; DB 1; Length 468;
Best Local Similarity 96.3%; Pred. No. 3.6e-27;
Matches 52; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MQEFGKLVGKPDAAETLKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 54
|||||
Db 66 MQEFGKLVGKPDAAETLKVMKQPCGVPDVAQFVLTGPNRWEQTHLYRIEN 119
|||||

RESULT 3

KCPGI

Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase

C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S15986; PID:G930269
 R;Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J.
 Matrix 11, 161-167, 1991
 A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of
 A;Reference number: S15986; MUID:91333421; PMID:1651440
 A;Accession: S15986
 A;Status: not compared with conceptual translation
 A;Molecule type: mRNA
 A;Residues: 1-469 <RIC>
 A;Cross-references: UNIPROT:P11692
 A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by
 R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P.
 Nucleic Acids Res. 18, 6703, 1990
 A;Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
 A;Reference number: S13597; MUID:91067477; PMID:2174547
 A;Accession: S13597
 A;Molecule type: mRNA
 A;Residues: 25-469 <CLA>
 A;Cross-references: EMBL:X54724; NID:G2016; PIDN:CAA38526.1; PID:G930269
 R;Li, J.; Brick, P.; Blow, D.M.
 submitted to the Brookhaven Protein Data Bank, April 1995
 A;Reference number: A65568; PDB:1FBL
 A;Content: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
 C;Comment: Procollagenase can be activated without removal of the activation peptide. St
 tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
 C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
 A;Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F;1-19/Domain: signal sequence #status predicted <SIG>
 F;20-469/Product: procollagenase #status predicted <PRO>
 F;20-99/Domain: activation peptide #status experimental <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PKN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status experimental

Query Match 92.5%; Score 270; DB 1; Length 469;
 Best Local Similarity 90.7%; Pred. No. 1.5e-25;
 Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 MQEFGKLVTKGKDAETLVKMKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 DB 67 MQQFFGLKVTGKDAETLVNWKPCGVPDVAEFLVTPGNPRWENTHLYRIEN 120

RESULT 4
 KCBOI
 Interstitial collagenase (EC 3.4.24.7) precursor - bovine
 N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue col
 C;Species: *Bos primigenius taurus* (cattle)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: S14654; S20336; S14655
 R;Tamura, M.; Shimokawa, H.; Sasaki, S.
 submitted to the EMBL Data Library, March 1991
 A;Reference number: S14654
 A;Accession: S14654
 A;Molecule type: mRNA
 A;Residues: 1-469 <TAM>
 A;Cross-references: UNIPROT:P28053; EMBL:X58256; NID:G259; PIDN:CAA41210.1; PID:G260
 R;Sudbeck, B.D.; Jeffrey, J.J.; Welgus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
 Arch. Biochem. Biophys. 293, 370-376, 1992
 A;Title: Purification and characterization of bovine interstitial collagenase and tissue
 A;Reference number: S20336; MUID:92161820; PMID:1311165
 A;Accession: S20336

A;Molecule type: protein
 A;Residues: 19-21, 'PP', 24-29, 'L', 31-34, 'LL', 37-39, 'P', 86-105, 'NPR', 109-112, 'D', 114-125 <P
 C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the
 C;Comment: Procollagenase can be activated without removal of the activation peptide. St
 tion peptide by other proteinases.
 C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of whi
 C;Function:
 A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
 F;1-18/Domain: signal sequence #status predicted <SIG>
 F;19-469/Product: procollagenase #status predicted <PRO>
 F;19-99/Domain: activation peptide #status predicted <ACT>
 F;60-261/Domain: matrix metalloproteinase homology <MMP>
 F;90-97/Region: autoinhibitory
 F;100-469/Product: interstitial collagenase #status predicted <MAT>
 F;272-466/Domain: hemopexin repeat homology <PKN>
 F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;120,143/Binding site: carboxylate (Asn) (covalent) #status predicted
 F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
 F;219/Active site: Glu #status predicted
 F;278-466/Disulfide bonds: #status predicted

Query Match 80.1%; Score 234; DB 1; Length 469;
 Best Local Similarity 81.5%; Pred. No. 4.2e-21;
 Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MQEFGKLVTKGKDAETLVKMKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 DB 67 MQQFFGLKVTGKDAETLVNWKPCGVPDVAEFLVTPGKSCWENTHLYRIEN 120

RESULT 5
 IS1267
 collagenase (EC 3.4.24.-) - bullfrog
 C;Species: *Rana catesbeiana* (bullfrog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: IS1267
 R;Oofusa, K.; Yomori, S.; Yoshizato, K.
 Int. J. Dev. Biol. 38, 345-350, 1994
 A;Title: Regionally and hormonally regulated expression of genes of collagen and collag
 A;Reference number: IS1267; MUID:95071832; PMID:7981043
 A;Accession: IS1267
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-384 <OOF>
 A;Cross-references: UNIPROT:Q11133; GB:S75623; NID:G913070; PIDN:AAB32661.1; PID:G913071
 C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprote
 C;Keywords: hydrolase; metalloproteinase; zinc; zymogen
 F;53-231/Domain: matrix metalloproteinase homology <MMP>
 F;236-381/Domain: hemopexin repeat homology <PKN>
 F;81,189,193,199/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
 F;189,193,199/Binding site: zinc, catalytic (His) (active) #status predicted
 F;190/Active site: Glu #status predicted

Query Match 79.3%; Score 231.5; DB 2; Length 384;
 Best Local Similarity 79.6%; Pred. No. 6.9e-21;
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MQEFGKLVTKGKDAETLVKMKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 DB 57 LKQFFGLKVTGKDAETLVNWKPCGVPDVAEFLVTPGNPRWENTHLYRIEN 109

RESULT 6
 KCHUN
 neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human
 N;Alternate names: matrix metalloproteinase 8
 C;Species: *Homo sapiens* (man)
 C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
 C;Accession: A37073; A61175; A6230; S09680; S11026; S19576; S27225; S32527; S624
 R;Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Stever
 J. Biol. Chem. 265, 11421-11424, 1990

A;Title: Human neutrophil collagenase. A distinct gene product with homology to other matrix metalloproteinases.
A;Reference number: A37073; MUID:90307647; PMID:2164002
A;Accession: A37073
A;Molecule type: mRNA
A;Residues: 1-467 <HAS>
A;Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G180618
R;Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.
Blood 77, 2731-2738, 1991
A;Title: Structure and expression of the cDNA encoding human neutrophil collagenase.
A;Reference number: A61175; MUID:91255696; PMID:1646048
A;Accession: A61175
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-31, 'I', '33-86', 'E', '88-467 <DEV>
A;Accession: B61175
A;Molecule type: protein
A;Residues: 263-264, 'X', '266-270', 'X', '272-273', 'X', '275', 'X', '277 <DE2>
R;Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V.
Biochemistry 29, 10628-10634, 1990
A;Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with
A;Reference number: A36230; MUID:91104978; PMID:2176876
A;Accession: A36230
A;Molecule type: protein
A;Residues: 'X', '88-87', 'X', '89-90', 'X', '92-97', 'X', '99-111', 'X', '113-120 <NAL>
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 189, 295-300, 1990
A;Title: Characterization and activation of procollagenase from human polymorphonuclear
A;Reference number: S09680; MUID:90249372; PMID:2159879
A;Accession: S09680
A;Molecule type: protein
A;Residues: 21-31, 'I', '33-39', 'I', '41-47', 'V', '49-53', 'I', '55-72', 'G', '74-86', 'E', '88-111', 'X', '113-120
A;Note: 67-Lys was also found
R;Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.
Biol. Chem. Hoppe-Seyler 371, 733, 1990
A;Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.
A;Reference number: S11026; MUID:91000455; PMID:2169766
A;Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990
A;Accession: S11026
A;Molecule type: protein
A;Residues: 21-31, 'I', '33-53', 'I', '55-72', 'G', '74-111', 'X', '113-140;183-203', 'X', '205-209;248-261
A;Note: 87-Glu was also found
R;Blaeser, J.; Knaeuper, V.; Osthus, A.; Reinke, H.; Tschesche, H.
Eur. J. Biochem. 202, 1223-1230, 1991
A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
A;Reference number: S19576; MUID:92111500; PMID:1662606
A;Accession: S19576
A;Molecule type: protein
A;Residues: 69-103 <BL2>
R;Blaeser, J.; Triefel, S.; Reinke, H.; Tschesche, H.
FEBS Lett. 313, 59-61, 1992
A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase.
A;Reference number: S27225; MUID:93050220; PMID:1330697
A;Accession: S27225
A;Molecule type: protein
A;Residues: 68-103 <BLA>
R;Knaeuper, V.; Osthus, A.; DeClerck, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H.
Biochem. J. 291, 847-854, 1993
A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
A;Reference number: S32527; MUID:93256897; PMID:8489511
A;Accession: S32527
A;Molecule type: protein
A;Residues: 100-112;263-276 <KN3>
R;Knaeuper, V.; Murphy, G.; Tschesche, H.
Eur. J. Biochem. 235, 187-191, 1996
A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
A;Reference number: S62608; MUID:96202934; PMID:8631328
A;Accession: S62608
A;Molecule type: protein
A;Residues: 21-39, 'I', '41-47', 'V', '49-122 <KN4>
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B.
submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A67078; PMID:1MNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', '106-149', 'G', '1

[illegible]

Biochemistry 37, 4699-4702, 1998
A>Title: Generation of an angiotensin-like fragment from plasminogen by stromelysin-1
A:Reference number: A58812; MUID:9548733; PMID:9548733
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, February 1997
A:Reference number: A58466; PDB:1HFS
A:Contents: annotation; X-ray crystallography, 1.70 angstroms, residues 105-160
R:Becker, J.W.; Marcy, A.I.; Kossz, L.L.; Axel, M.G.; Burbaum, J.J.; Fitzgerald, P.M.D.
Protein Sci. 4, 1966-1976, 1995
A>Title: Stromelysin-1: three-dimensional structure of the inhibited catalytic domain an
A:Reference number: A58814; MUID:96117647; PMID:9535233
A:Contents: annotation; X-ray crystallography, 1.70 angstroms
R:Marcy, A.I.; Eiberger, L.L.; Harrison, R.; Chan, H.K.; Hutchinson, N.I.; Hagmann, W.K.
Biochemistry 30, 6476-6483, 1991
A>Title: Human fibroblast stromelysin catalytic domain: expression, purification, and ch
A:Reference number: A39589; MUID:91274298; PMID:1647201
A:Contents: annotation
R:Becker, J.W.
submitted to the Brookhaven Protein Data Bank, August 1995
A:Reference number: A66637; PDB:1SLM
A:Contents: annotation; X-ray crystallography, 1.90 angstroms, residues 33-47;57-267
R:Gooley, P.R.; O'Connell, J.F.
submitted to the Brookhaven Protein Data Bank, March 1995
A:Reference number: A67284; PDB:2SRT
A:Contents: annotation; Confirmation by (1)H-NMR, residues 100-272
R:Gooley, P.R.; Johnson, B.A.; Marcy, A.I.; Cuca, G.C.; Salowe, S.P.; Hagmann, W.K.; Esser
Biochemistry 32, 13098-14008, 1993
A>Title: Secondary structure and zinc ligation of human recombinant short-form stromelysin;
A:Reference number: A58815; MUID:94059987; PMID:8241164
A:Contents: annotation; confirmation by (1)H-NMR
C:Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C:Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whic
C:Genetics:
A:Gene: GDB:MMP3; STMY; STMV1
A:Cross-references: GDB:120727; OMIM:185250
A:Map position: 11q23-11q23
C:Function:
A>Note: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl side
Plasminogen to yield a fragment with angiotensin activity
C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotein
C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallopro
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-477/Product: prostromelysin 1 #status experimental <PRO>
F:18-99/Domain: activation peptide #status experimental <ACT>
E:60-264/Domain: matrix metalloproteinase homology <MMP>
F:100-477/Product: stromelysin 1 #status experimental <MAT>
F:284-477/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His)
F:120/Binding site: carboxylate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F:219/Active site: Glu #status predicted
F:290-477/Disulfide bonds: #status predicted

Query Match 64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred No. 1.6e-15;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTCKPAETLKVMPKRCGPDVAQFVLTEGNPRWEQHTLYRIEN 54
| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 67 MQKFLGLEVTCKLSDTLEVMRKPCGPDVGHFRTFGIPKWKTHLTIRIVN 120

RESULT 9
KCRES1
N:Stromelysin 1 (EC 3.4.24.17) precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: A37306; A29157
R:Finni, M.E.; Karmilowicz, M.J.; Ruby, P.L.; Beeman, A.M.; Borges, K.A.; Brincknerhoff, C
Arthritis Rheum. 30, 1254-1264, 1987

RESULT 12

KCRTIH
stromelysin 1 (EC 3.4.24.17) precursor - rat
N/Alternate names: collagenase activating protein; matrix metalloproteinase 3 (MMP3); pro-
C/Species: Rattus norvegicus (Norway rat)
C/Date: 13-Aug-1986 #sequence_revision 13-Aug-1986 #text_change 09-Jul-2004
C/Accession: A00997; PS0150; S22767
R/Matrisian, L.M.; Glaichenhaus, N.; Gesnel, M.C.; Breathnach, R.
EMBO J. 4, 1435-1440, 1985
A/Title: Epidermal growth factor and oncogenes induce transcription of the same cellular
A/Reference number: A00997; MUID:85284930; PMID:3875482
A/Accession: A00997
A/Molecule type: mRNA
A/Residues: 1-475 <NAI>
A/Cross-references: UNIPROT:P03957; GB:X02601; NID:G57460; PIDN:CAA26448.1; PID:G57461
R/Umenishi, F.; Yasumitsu, H.; Ashida, Y.; Yamauti, J.; Umeda, M.; Miyazaki, K.
J. Biochem. 108, 537-543, 1990
A/Title: Purification and properties of extracellular matrix-degrading metallo-proteinase
A/Reference number: PS0150; MUID:91154156; PMID:1963430
A/Accession: PS0150
A/Molecule type: protein
A/Residues: 19-20,'X',22-28;110-112,'X',114-115,'X',117,'X',119;309-325 <UME>
R/Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A/Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A/Reference number: A26403; MUID:87146421; PMID:3547333
A/Contents: annotation; introns
A/Note: Intron positions were determined by comparison of the previously reported cDNA s
R/Sanchez-Lopez, R.; Nicholson, R.; Gesnel, M.C.; Matrisian, L.M.; Breathnach, R.
J. Biol. Chem. 263, 11892-11899, 1988
A/Title: Structure-function relationships in the collagenase family member transin.
A/Reference number: S22767; MUID:98298869; PMID:2841336
A/Contents: annotation; active site; activation
A/Note: molecules with mutations in the autoinhibitory region showed a much increased te
R/Park, A.J.; Matrisian, L.M.; Kells, A.F.; Pearson, R.; Yuan, Z.; Navre, M.
J. Biol. Chem. 266, 1584-1590, 1991
A/Title: Mutational analysis of the transin (rat stromelysin) autoinhibitor region demon
A/Reference number: A43028; MUID:91107652; PMID:1988438
A/Contents: annotation; autoinhibitory region
C/Comment: Arg-89 and Cys-92 are essential for maintaining latency
C/Comment: This enzyme degrades various extracellular matrix proteins, including fibron
C/Comment: Stromelysin 1 hydrolyzes peptide bonds in plasminogen to yield a fragment wit
C/Comment: Stromelysin 1 activates its proenzyme after cleavage(s) within the activation
C/Comment: Prostromelysin is found in glycosylated and unglycosylated forms, both of whi
C/Genetics: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
A/Introns: 33/3; 115/2; 165/1; 207/1; 262/1; 310/2; 355/1; 408/2; 443/1
C/Function:
A/Description: endopeptidase preferentially hydrolyzing peptide bonds on the carboxyl si
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-475/Product: prostromelysin 1 #status predicted <PRO>
F;18-97/Domain: activation peptide #status predicted <ACT>
F;58-262/Domain: matrix metalloproteinase homology <MMP>
F;88-95/Region: autoinhibitory
F;98-475/Product: stromelysin 1 #status predicted <MAT>
F;282-475/Domain: hemopexin repeat homology <PXN>
F;90,216,220,226/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;118/Binding site: carboxylate (Asn) (covalent) #status predicted
F;216,220,226/Binding site: zinc, catalytic (His) (active) #status predicted
F;217/Active site: Glu #status experimental
F;288-475/Disulfide bonds: #status predicted

Query Match 58.9%; Score 172; DB 1; Length 475;
Best Local Similarity 53.7%; Pred. No. 2e-13;
Matches 29; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 65 MQKFLGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 118

RESULT 13

JC5743
matrix metalloproteinase (EC 3.4.24.-) precursor - pig
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 09-Dec-1997 #sequence_revision 23-Jan-1998 #text_change 09-Jul-2004
C/Accession: JC5743
R/Bartlett, J.D.; Simmer, J.P.; Xue, J.; Margolis, H.C.; Moreno, E.C.
Gene 183, 123-128, 1996
A/Title: Molecular cloning and mRNA tissue distribution of a novel matrix metalloprotein
A/Reference number: JC5743; MUID:97145286; PMID:8996096
A/Accession: JC5743
A/Molecule type: mRNA
A/Residues: 1-483 <BAR>
A/Cross-references: UNIPROT:P79287; GB:U54825; NID:G1800212; PIDN:AAB41396.1; PID:G18002
A/Experimental source: enamel organ
C/Comment: This enzyme plays a role in enamel biomineralization and development.
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: hydrolase; metalloproteinase; zinc
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-483/Product: matrix metalloproteinase #status predicted <MAT>
F;68-271/Domain: matrix metalloproteinase homology <MMP>
F;280-483/Domain: hemopexin repeat homology <PXN>
F;100,226,230,236/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;226,230,236/Binding site: zinc, catalytic (His) #status predicted
F;227/Active site: Glu #status predicted

Query Match 58.9%; Score 172; DB 2; Length 483;

Best Local Similarity 59.8%; Pred. No. 2e-13;
Matches 31; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 52

Db 75 LQAFGLRVTKGLDRITMDVIKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 126

RESULT 14

S29243
interstitial collagenase (EC 3.4.24.7) precursor - mouse
N/Alternate names: matrix metalloproteinase 1 (MMP1)
C/Species: Mus musculus (house mouse)
C/Date: 22-Nov-1993 #sequence_revision 03-Aug-1995 #text_change 09-Jul-2004
C/Accession: S29243
R/Henriet, P.; Rousseau, G.G.; Eckhout, Y.
FEBS Lett. 310, 175-178, 1992
A/Title: Cloning and sequencing of mouse collagenase cDNA. Divergence of mouse and rat c
A/Reference number: S29243; MUID:93011910; PMID:11383028
A/Accession: S29243
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-472 <HEN>
A/Cross-references: UNIPROT:P33435; EMBL:X66473; NID:G53603; PIDN:CAA47102.1; PID:G53604
C/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C/Keywords: hydrolase; metalloproteinase; zinc; zymogen
F;65-268/Domain: matrix metalloproteinase homology <MMP>
F;279-472/Domain: hemopexin repeat homology <PXN>
F;97,223,227,233/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status
F;223,227,233/Binding site: zinc, catalytic (His) (active) #status predicted
F;224/Active site: Glu #status predicted

Query Match 57.5%; Score 168; DB 2; Length 472;

Best Local Similarity 57.4%; Pred. No. 6.2e-13;
Matches 31; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54

Db 72 MQSFFGLEVTGKLDLDTLDMRKPCGVPDVGSEYVFPFRLKWSQTNLYRIYN 125

RESULT 15

KCRTS2
stromelysin 2 (EC 3.4.24.22) precursor - rat

N;Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: B26403; A11775; S26498
R;Breathnach, R.; Matrisian, L.M.; Gesnel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A;Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A;Reference number: A26403; MUID:87146421; PMID:3547333
A;Accession: B26403
A;Molecule type: mRNA
A;Residues: 1-476 <BRE>
A;Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:q57389
A;Note: intron positions were determined by comparison of the cDNA sequence to genomic g
R;Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas
J. Biol. Chem. 267, 1099-1103, 1992
A;Title: Molecular cloning and characterization of v-mos-activated transformation-associ
A;Reference number: A11775; MUID:92112748; PMID:1370458
A;Accession: A11775
A;Molecule type: mRNA
A;Residues: 1-476 <CHA>
A;Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:g207151
A;Note: sequence extracted from NCBI backbone (NCBIP:76184)
R;de Voege, M.W.; Mukherjee, B.B.
Oncogene 7, 109-119, 1992
A;Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra
A;Reference number: S26496; MUID:92158347; PMID:1741158
A;Accession: S26498
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 31-103, 'L', 241-242, 'TQMEKPH', 251, 'L', 253-254, 'CE', 293-294, 'L', 296 <DEV>
A;Cross-references: EMBL:X64020
C;Genetics:
A;Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallopro
F;1-17/Domain: signal sequence #status predicted <SIG>
F;18-476/Product: prostromelysin 2 #status predicted <PRO>
F;18-99/Domain: activation peptide #status predicted <ACT>
F;60-264/Domain: matrix metalloproteinase homology <MMP>
F;90-97/Region: autoinhibitory
F;100-476/Product: stromelysin 2 #status predicted <MAT>
F;283-476/Domain: hemopexin repeat homology <PXN>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;120/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;219/Active site: Glu #status predicted
F;289-476/disulfide bonds: #status predicted

Query Match 57.2%; Score 167; DB 1; Length 476;
Best Local Similarity 51.9%; Pred. No. 8.4e-13;
Matches 28; Conservative 13; Mismatches 13; Indels 0; Gaps 0;

[illegible]

Search completed: May 27, 2005, 07:13:34
Job time : 21.4231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 94.5 Seconds
(without alignments)

292.617 Million cell updates/sec

Title: US-10-032-376a-9

Perfect score: 292

Sequence: 1 MQEFGGLKVTGKPDATLKV.....VLTEGNPRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	292	100.0	469	1 MM01 HUMAN	P03956 homo sapien
2	283	96.9	468	1 MM01 RABIT	P13943 oryctolagus
3	279	95.5	469	1 MM01 HORSE	O9xs25 equus caball
4	270	92.5	469	1 MM01 PIG	P21692 sus scrofa
5	234	80.1	469	1 MM01 BOVIN	P28053 bos taurus
6	231.5	79.3	384	1 MM01 RANCA	Q11133 rana catesb
7	214	73.3	467	1 MM08 HUMAN	P22894 homo sapien
8	204	69.9	205	2 Q810Z2	Q810Z2 mus musculus
9	204	69.9	463	2 Q9EPL6	Q9EPL6 mus musculus
10	204	69.9	464	2 Q9EPL5	Q9EPL5 mus musculus
11	196	67.1	466	1 MM08 RAT	O88766 rattus norv
12	189	64.7	476	1 MM10 HUMAN	P09238 homo sapien
13	189	64.7	477	1 MM03 HUMAN	P08254 homo sapien
14	189	64.7	478	2 Q6Y4Q5	Q6Y4Q5 canis fami
15	186	63.7	145	2 Q9N283	Q9N283 bos taurus
16	186	63.7	393	2 Q8M118	Q8M118 felis silve
17	186	63.7	478	1 MM03 RABIT	P28863 oryctolagus
18	184	63.0	252	2 Q6PMQ3	Q6PMQ3 xenopus lae
19	184	63.0	259	2 Q7ZT19	Q7ZT19 xenopus lae
20	183	62.7	472	2 Q93342	Q93342 gallus gall
21	183	62.7	477	1 MM03 HORSE	O28397 equus cabal
22	181	62.0	466	2 Q7SVX1	Q7SVX1 xenopus lae
23	180	61.6	259	2 Q7SZT5	Q7SZT5 xenopus lae
24	179	61.3	458	2 Q6DCN8	Q6DCN8 xenopus lae
25	178	61.0	258	2 Q7SZS8	Q7SZS8 xenopus lae
26	178	61.0	259	2 Q6DF35	Q6DF35 xenopus tro
27	178	61.0	481	1 MM20 BOVIN	O18767 bos taurus
28	176	60.3	465	2 Q8C309	Q8C309 mus musculus
29	176	60.3	465	2 Q8C330	Q8C330 mus musculus
30	176	60.3	471	1 MM13 RABIT	O62806 oryctolagus
31	174	59.6	167	2 Q7ZWD0	Q7ZWD0 brachydanio

32	174	59.6	482	1 MM20 MOUSE	P57748 mus musculus
33	173	59.2	476	1 MM10 MOUSE	O55123 mus musculus
34	173	59.2	477	1 MM03 MOUSE	P28862 mus musculus
35	173	59.2	479	2 Q922K6	Q922K6 mus musculus
36	172	58.9	475	1 MM03 RAT	P03957 rattus norv
37	172	58.9	483	1 MM20 HUMAN	O60882 homo sapien
38	172	58.9	483	1 MM20 PIG	P79287 sus scrofa
39	172	58.9	483	2 Q6DKT9	Q6DKT9 homo sapien
40	171	58.6	471	2 Q98859	Q98859 cynops pyrr
41	170	58.2	139	2 Q9GM68	Q9GM68 sus scrofa
42	168	57.5	452	2 Q9TT82	Q9TT82 canis fami
43	168	57.5	455	1 MM08 MOUSE	O70138 mus musculus
44	168	57.5	472	1 MM13 MOUSE	P33435 mus musculus
45	167.5	57.4	475	2 Q9DEE0	Q9DEE0 oncorhynch

ALIGNMENTS

RESULT 1

ID	MM01_HUMAN	STANDARD	PRT	469 AA
AC	P03956; P08156;			
DT	23-OCT-1986 (Rel. 02, Created)			
DT	01-DEC-1992 (Rel. 24, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1) (Fibroblast collagenase).			
DE	Names=MMP1; Synonyms=CLG;			
GN	Homo sapiens (Human).			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OC	NCBI_TaxID=9606;			
OX	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=90352587; PubMed=2167156;			
RX	Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A., Stetler-Stevenson W.G.;			
RA	"Cloning and characterization of human tumor cell interstitial collagenase";			
RT	Cancer Res. 50:5431-5437(1990).			
RL	[2]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=87156645; PubMed=3030290;			
RX	Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A., Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;			
RA	"Comparison of human stromelysin and collagenase by cloning and sequence analysis";			
RT	Biochem. J. 240:913-916(1986).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=86196089; PubMed=3009463;			
RX	Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A., Eisen A.Z.;			
RA	"Human fibroblast collagenase. Complete primary structure and homology to an oncogene transformation-induced rat protein.";			
RT	J. Biol. Chem. 261:6600-6605(1986).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A., Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D., Heller R., Davis R.W.;			
RA	Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Ovary;			
RC	MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RX	Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D., Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heife F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedino T.B., Toehiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Boeak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzyzinski M.I., Skaleka U., Smalilus D.E.,
RA Schnersch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RP SEQUENCE OF 1-35 FROM N.A.
RX MEDLINE=87257941; PubMed=3037355;
RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
RA Herrlich P.;
RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
RT collagenase gene is mediated by an inducible enhancer element located
RT in the 5'-flanking region.";
RL Mol. Cell. Biol. 7:2256-2266(1987).
RN [7]
RP SEQUENCE OF 1-70 FROM N.A.
RC TTSUE-Synovial cell;
RX MEDLINE=87109799; PubMed=3027129;
RA Brinckhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
RT "Molecular cloning of human synovial cell collagenase and selection of
RT a single gene from genomic DNA.";
RL J. Clin. Invest. 79:542-546(1987).
RN [8]
RP SEQUENCE OF 100-112 AND 270-287.
RC TTSUE=Fibroblast;
RX MEDLINE=87194799; PubMed=3032950;
RA Clark I.M., Cawston T.E.;
RT "Fragments of human fibroblast collagenase. Purification and
RT characterization.";
RL Biochem. J. 263:201-206(1989).
RN [9]
RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
RX MEDLINE=87194799; PubMed=3032950;
RA McKerrow J.H.;
RT "Human fibroblast collagenase containing an amino acid sequence
RT homologous to the zinc-binding site of Serratia protease.";
RL J. Biol. Chem. 262:5943-5943(1987).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
RX MEDLINE=95384760; PubMed=7656013;
RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
RA Brown P.A., Johnson W.H., Murray E.J.;
RT "Structure of the catalytic domain of human fibroblast collagenase
RT complexed with an inhibitor.";
RL Nat. Struct. Biol. 1:106-110(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
RX MEDLINE=94304829; PubMed=8031754;
RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
RT "Crystal structures of recombinant 19-kDa human fibroblast collagenase
RT complexed to itself.";
RL Biochemistry 33:8207-8217(1994).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
RX MEDLINE=94105765; PubMed=8278810;
RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
RA Jordan S.R.;
RT "Structure of the catalytic domain of fibroblast collagenase complexed
RT with an inhibitor.";
RL Science 263:375-377(1994).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
RX MEDLINE=94377426; PubMed=8090713;
RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
RT "1.56-A structure of mature truncated human fibroblast collagenase.";
RN Proteins 19:98-109(1994).
RN [14]
RP STRUCTURE BY NMR OF 101-269.
RX MEDLINE=98145213; PubMed=9484219; DOI=10.1021/bi972181w;
RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
RA Powers R.;
RT "High-resolution solution structure of the inhibitor-free catalytic
RT fragment of human fibroblast collagenase determined by
RT multidimensional NMR.";
RL Biochemistry 37:1495-1504(1998).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- DOMAIN: There are two distinct domains in this protein; the
CC catalytic N-terminal, and the C-terminal which is involved in
CC substrate specificity and in binding TIMP (tissue inhibitor of
CC metalloproteinases).
CC -!- PTM: Undergoes autolytic cleavage to two major forms (22 kDa and
CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
CC can act as activator for collagenase.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
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CC -----
DR EMBL; X05231; CAA28858.1; -;
DR EMBL; M13509; AAA35699.1; -;
DR EMBL; M16567; AAA52033.1; -;
DR EMBL; U78045; AAB36941.1; -;
DR EMBL; BC013875; AAH13875.1; -;
DR EMBL; M15996; AAA35700.1; -;
DR EMBL; X54925; CAA38691.1; -;
DR PIR; A37308; KCHUL.
DR PDB; 1AYK; NMR; @=101-269.
DR PDB; 1CGE; X-ray; @=102-269.
DR PDB; 1CGF; X-ray; A/B=102-263.
DR PDB; 1CGL; X-ray; A/B=101-269.
DR PDB; 1HFC; X-ray; @=101-269.
DR PDB; 2AYK; NMR; @=101-269.
DR PDB; 2TCL; X-ray; @=101-269.
DR PDB; 3AYK; NMR; A=101-269.
DR PDB; 4AYK; NMR; A=101-269.
DR MEROPS; M10.001; -;
DR GlycoSuiteDB; P03956; -;
DR Genew; HGNC:7155; MMP1.
DR H-InvDB; HIX0010067; -;
DR MIM; 120353; -;
DR GO; GO:0008133; F:collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0006508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.

CC	EMBL; M17823; AAB88016.1; --
DR	EMBL; M17820; AAB88016.1; JOINED.
DR	EMBL; M17821; AAB88016.1; JOINED.
DR	EMBL; M17822; AAB88016.1; JOINED.
DR	EMBL; M19240; AAB88016.1; JOINED.
DR	EMBL; M25663; AAA31203.1; --

RESULT 3
MM01 HORSE

ID MM01 HORSE STANDARD; PRT; 469 AA.
 AC Q9XZ5;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).
 DE metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Equus caballus (Horse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 OX NCBI_TaxID=9796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Richardson D.W.;
 RT "Cloning and expression of equine matrix metalloproteinase 1 (interstitial collagenase).";
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in the helical domain. Also cleaves collagens of types VII and X. collagen. Cleavage of the triple helix of collagen at about three-quarters of the length of the molecule from the N-terminus, at 775-Gly-[Ile-776 in the alpha-1(I) chain. Cleaves synthetic substrates and alpha-macroglobulins at bonds where P1' is a hydrophobic residue.
 CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By similarity).
 CC -!- ENZYME REGULATION: Can be activated without removal of the activation peptide.
 CC -!- SIMILARITY: Belongs to the peptidase M10A family.
 CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AF148882; AAD38030.1; --
 DR HSP; P03956; IAYK.
 DR MEROPS; M10.001; --
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept M10A_M12B.
 DR InterPro; IPR006025; Pept M_Zn_BS.
 DR InterPro; IPR006026; Peptidase M.
 DR InterPro; IPR009070; PGD like.
 DR Pfam; PF00045; Hemopexin_4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR SMART; SM00120; HK; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 18 By similarity.
 FT PROPEP 19 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT METAL 124 124 Calcium 1 (By similarity).
 FT METAL 158 158 Calcium 2 (By similarity).
 FT METAL 168 168 Zinc 1 (By similarity).
 FT METAL 170 170 Zinc 1 (By similarity).
 FT METAL 175 175 Calcium 3 (By similarity).
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen) (By similarity).

FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen) (By similarity).
 FT METAL 183 183 Zinc 1 (By similarity).
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By similarity).
 FT METAL 194 194 Calcium 2 (By similarity).
 FT METAL 196 196 Zinc 1 (By similarity).
 FT METAL 198 198 Calcium 3 (By similarity).
 FT METAL 199 199 Calcium 1 (By similarity).
 FT METAL 201 201 Calcium 3 (By similarity).
 FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
 FT ACT_SITE 219 219 By similarity.
 FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
 FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By similarity).
 FT DISULFID 278 466 By similarity.
 SQ SEQUENCE 469 AA; 54001 MW; ABE6760AB2C529CA CRC64;
 Query Match 95.5%; Score 279; DB 1; Length 469;
 Best Local Similarity 94.4%; Pred. No. 1.8e-27;
 Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MOEFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQHLTYRIEN 54
 DB 67 MOEFGLKVTGPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQHLTYRIEN 120
 RESULT 4
 MM01_PIG STANDARD; PRT; 469 AA.
 AC P21692;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=9133421; PubMed=1651440;
 RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
 RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of expression of RNA in vitro by various cytokines.";
 RL Matrix 11:161-167(1991).
 RN [2]
 RP SEQUENCE OF 25-469 FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=91067477; PubMed=2174547;
 RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
 RT "Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR."
 RL Nucleic Acids Res. 18:6703-6703(1990).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
 RX MEDLINE=96173003; PubMed=8590015; DOI=10.1016/S0969-2126(01)00188-5;
 RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A., Clark I.M., Blegg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
 RT "Structure of full-length porcine synovial collagenase reveals a C-

terminal domain containing a calcium-linked, four-bladed beta-propeller.";
 Structure 3:541-549(1995).
 [4]
 RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
 RX MEDLINE=95142615; PubMed=784605; DOI=10.1006/abbi.1995.1018;
 RA Clark I.M., Mitchell R.E., Powell L.K., Biggs H.F., Cawston T.E.,
 O'Hare M.C.;
 RT "Recombinant porcine collagenase: purification and autolysis.";
 RL Arch. Biochem. Biophys. 316:123-127(1995).
 CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where Pl' is a
 CC hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -1- PTM: Undergoes autolytic cleavage to produce a N-terminal fragment
 CC having reduced collagenolytic activity.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X54724; CAA38526.1; -;
 DR PIR; S15986; KCPGI.
 DR PDB; 1FBL; X-ray; @=100-469.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR009070; PGSD like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
 KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 19
 FT PROPEP 20 99 Activation peptide.
 FT CHAIN 100 469 Interstitial collagenase.
 FT CHAIN 100 258 18 kDa interstitial collagenase.
 FT DOMAIN 275 469 Hemopexin-like.
 FT SITE 92 92 Cysteine switch (Potential).
 FT SITE 258 259 Cleavage (autolytic).
 FT METAL 124 124 Calcium 1.
 FT METAL 158 158 Calcium 2.
 FT METAL 168 168 Zinc 1.
 FT METAL 170 170 Zinc 1.
 FT METAL 175 175 Calcium 3.
 FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
 FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
 FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
 FT METAL 183 183 Zinc 1.
 FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
 FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
 FT METAL 194 194 Zinc 1.
 FT METAL 196 196 Zinc 1.
 FT METAL 198 198 Calcium 3.
 FT METAL 199 199 Calcium 1.
 FT METAL 201 201 Calcium 3.
 FT METAL 218 218 Zinc 2 (catalytic).
 FT ACT_SITE 219 219 Zinc 2 (catalytic).
 FT METAL 222 222 Zinc 2 (catalytic).
 FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
 FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
 FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
 FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
 FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
 FT DISULFID 478 466 N-linked (GlcNAc. .) (Potential).
 FT CARBOHYD 120 120
 FT STRAND 101 102
 FT TURN 104 105
 FT STRAND 113 118
 FT TURN 123 124
 FT HELIX 127 142
 FT TURN 143 144
 FT STRAND 148 152
 FT STRAND 159 164
 FT STRAND 182 184
 FT TURN 190 193
 FT STRAND 195 198
 FT TURN 199 200
 FT STRAND 204 204
 FT STRAND 211 211
 FT HELIX 212 223
 FT TURN 224 225
 FT STRAND 226 227
 FT TURN 232 233
 FT TURN 235 236
 FT HELIX 250 260
 FT TURN 277 278
 FT STRAND 280 281
 FT STRAND 286 290
 FT TURN 291 292
 FT STRAND 293 298
 FT TURN 299 300
 FT STRAND 301 305
 FT STRAND 313 316
 FT HELIX 317 320
 FT STRAND 330 334
 FT TURN 335 338
 FT STRAND 339 344
 FT TURN 345 346
 FT STRAND 347 352
 FT TURN 353 354
 FT STRAND 355 356
 FT TURN 358 359
 FT STRAND 362 363
 FT HELIX 364 368
 FT TURN 372 373
 FT STRAND 379 383
 FT TURN 384 387
 FT STRAND 388 393
 FT TURN 394 395
 FT STRAND 396 401
 FT TURN 402 405
 FT STRAND 406 407
 FT STRAND 413 414
 FT TURN 415 418
 FT TURN 420 421
 FT STRAND 428 432
 FT TURN 433 434
 FT STRAND 435 440
 FT TURN 441 442
 FT STRAND 443 448
 FT TURN 449 452
 FT STRAND 453 459

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FT TURN 460 461
FT HELIX 462 464
FT TURN 465
SQ SEQUENCE 469 AA; 53666 MW; 7952D72B2753F682 CRC64;

Query Match 92.5%; Score 270; DB 1; Length 469;
Best Local Similarity 90.7%; Pred. No. 2.6e-26;
Matches 49; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
||:|||||
Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

RESULT 5
MM01_BOVIN STANDARD; PRT; 469 AA.
ID MM01_BOVIN
AC P28053;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Periodontium fibroblast;
RX MEDLINE=95201294; PubMed=7894061;
RA Tamura M., Shimokawa H., Sasaki S.;
RT "Primary structure of bovine interstitial collagenase deduced from
RT cDNA sequence.";
RL DNA Seq. 5:63-66(1994).
RN [2]
RP SEQUENCE OF 19-39 AND 85-125.
RX PubMed=131165;
RA Sudbeck B.D., Jeffrey J.J., Welgus H.G., Mecham R.P., McCourt D.,
RA Parks W.C.;
RT "Purification and characterization of bovine interstitial collagenase
RT and tissue inhibitor of metalloproteinases.";
RL Arch. Biochem. Biophys. 293:370-376(1992).
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagenially one bond in native
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X58256; CAA41210.1; -.
CC FIR; S14654; KCBO1.
CC HSP; P03956; 1HFC.
CC MEROPS; M10.001; -.
CC InterPro; IPR000585; Hemopexin.

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DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGBD like.
DR Pfam; PF00445; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZMCG; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Direct protein sequencing;
KW Extracellular matrix; Glycoprotein; Hydrolase; Metal-binding;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 18 Activation peptide.
FT PROPEP 19 99 Interstitial collagenase.
FT CHAIN 100 469 Hemopexin-like.
FT DOMAIN 275 469 Cysteine switch (Potential).
FT SITE 92 92 Calcium 1 (By similarity).
FT METAL 124 124 Calcium 2 (By similarity).
FT METAL 158 158 Zinc 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Calcium 3 (By similarity).
FT METAL 175 175 Calcium 3 (via carbonyl oxygen) (By
FT METAL 176 176 similarity).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen) (By
FT METAL 180 180 similarity).
FT METAL 183 183 Calcium 3 (via carbonyl oxygen) (By
FT METAL 190 190 Zinc 1 (By similarity).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen) (By
FT METAL 194 194 similarity).
FT METAL 196 196 Calcium 2 (By similarity).
FT METAL 198 198 Zinc 1 (By similarity).
FT METAL 199 199 Calcium 3 (By similarity).
FT METAL 201 201 Calcium 3 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen) (By
FT METAL 329 329 similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By
FT METAL 427 427 similarity).
FT DISULFID 278 466 By similarity.
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CONFLICT 22 23 AT -> FP (in Ref. 2).
FT CONFLICT 30 30 D -> L (in Ref. 2).
FT CONFLICT 35 36 KK -> LL (in Ref. 2).
FT CONFLICT 85 85 N -> F (in Ref. 2).
FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
FT CONFLICT 113 113 N -> D (in Ref. 2).
SQ SEQUENCE 469 AA; 53354 MW; B4A5504CE24BD7B5 CRC64;

Query Match 80.1%; Score 234; DB 1; Length 469;
Best Local Similarity 81.5%; Pred. No. 1.2e-21;
Matches 44; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

OY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
||:|||||
Db 67 MQQFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLYRIEN 120

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RESULT 6
 ID MM01 RANCA STANDARD; PRT; 384 AA.
 AC Q1113;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 DE metalloproteinase-1) (MMP-1) (TCL).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8400;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skin;
 RX Medline=9501832; PubMed=7981043;
 RA Cofusa K., Yomori S., Yoshizato K.;
 RT "Regionally and hormonally regulated expression of genes of collagen
 and collagenase in the anuran larval skin.";
 RL Int. J. Dev. Biol. 38:345-350(1994).
 CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 collagen. Cleavage of the triple helix of collagen at about three-
 quarters of the length of the molecule from the N-terminus, at
 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 substrates and alpha-macroglobulins at bonds where P1' is a
 hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 similarity).
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 activation peptide (By similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.

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 or send an email to license@isb-sib.ch).

 DR EMBL; S75623; AAB32661.1; -;
 DR EMBL; I51267; I51267.
 DR HSSP; P21692; IFBL.
 DR MEROPS; M10.001; -;
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR009070; FGSD_like.
 DR Pfam; PF00045; Hemopexin; 2.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRILIX.
 DR SMART; SM00120; HX; 2.
 DR SMART; SM00235; ZNMC; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1;
 KW Hydrolyase; Metal-binding; Collagen degradation; Extracellular matrix;
 FT SIGNAL 1 25 Potential.
 FT PROPEP 26 88 Activation peptide (Potential).
 FT CHAIN 89 384 Interstitial collagenase.
 FT DOMAIN 239 384 Hemopexin-like.
 FT SITE 81 81 Cysteine switch (Potential).
 FT METAL 113 113 Calcium 1 (By similarity).
 FT METAL 129 129 Calcium 2 (By similarity).
 FT METAL 139 139 Zinc 1 (By similarity).
 FT METAL 141 141 Zinc 1 (By similarity).
 RP SEQUENCE OF 21-103.

FT METAL 146 146 Calcium 3 (By similarity).
 FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By
 similarity).
 FT METAL 154 154 Zinc 1 (By similarity).
 FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By
 similarity).
 FT METAL 165 165 Calcium 2 (By similarity).
 FT METAL 167 167 Zinc 1 (By similarity).
 FT METAL 169 169 Calcium 3 (By similarity).
 FT METAL 170 170 Calcium 1 (By similarity).
 FT METAL 172 172 Calcium 3 (By similarity).
 FT METAL 189 189 Zinc 2 (catalytic) (By similarity).
 FT ACT_SITE 190 190 By similarity.
 FT METAL 193 193 Zinc 2 (catalytic) (By similarity).
 FT METAL 199 199 Zinc 2 (catalytic) (By similarity).
 FT METAL 249 249 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 277 277 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT METAL 347 347 Calcium 4 (via carbonyl oxygen) (By
 similarity).
 FT DISULFID 242 381 By similarity.
 SQ SEQUENCE 384 AA; 43582 MW; A5B5E2FB32239DF CRC64;
 Query Match 79.3%; Score 231.5; DB 1; Length 384;
 Best Local Similarity 79.6%; Pred. No. 2.1e-21;
 Matches 43; Conservative 5; Mismatches 5; Indels 1; Gaps 1;
 QY 1 MQEFGKLVTKGPDASTLVKMKQPCGVPDVAQFVLTGPNRQTHLTTRIEN 54
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 DB 57 LKQFFGLKVTGKPDASTLVKMKQPCGVPDVAQFVLTGPNRQTHLTTRIEN 109
 ::::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 7
 ID MM08 HUMAN STANDARD; PRT; 467 AA.
 AC P22894;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
 DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).
 GN Name=MMP8; Synonyms=CLG1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.
 RC TISSUE=Neutrophils;
 RX Medline=90307647; PubMed=2164002;
 RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,
 RA Spinella D.G., Stevens R.M., Mainardi C.L.;
 RT "Human neutrophil collagenase. A distinct gene product with homology
 RT to other matrix metalloproteinases.";
 RL J. Biol. Chem. 265:11421-11424(1990).
 RN [2]
 RP SEQUENCE OF 21-140.
 RC TISSUE=Neutrophils;
 RX Medline=90249372; PubMed=2159879;
 RA Knauper V., Kraemer S., Reinke H., Teschesche H.;
 RT "Characterization and activation of procollagenase from human
 RT polymorphonuclear leucocytes N-terminal sequence determination of the
 RL proenzyme and various proteolytically activated forms.";
 RN Eur. J. Biochem. 189:295-300(1990).
 RN [3]
 RP SEQUENCE OF 21-103.

RC TISSUE=Neutrophils;
RX MEDLINE=92111500; PubMed=1662606;
RA Blaaser J., Knaeuper V., Oschues A., Reinke H., Tschesche H.;
RT "Mercurial activation of human polymorphonuclear leucocyte
RT procollagenase.";
RL Eur. J. Biochem. 202;1223-1230(1991).
RN [4]
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
RC TISSUE=Neutrophils;
RX MEDLINE=91104978; PubMed=2176876;
RA Maliya S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,
RT Birkedal-Hansen H., van Wart H.E.;
RA "Characterization of 58-kilodalton human neutrophil collagenase:
RT comparison with human fibroblast collagenase.";
RL Biochemistry 29:10628-10634(1990).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=90380298; PubMed=2169256;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";
RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).
RN [6]
RP ERRATUM.
RX MEDLINE=9100455; PubMed=2169766;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).
RN [7]
RP CYSTEINE-SWITCH MECHANISM.
RX MEDLINE=93050220; PubMed=1330697; DOI=10.1016/0014-5793(92)81184-N;
RA Blaaser J., Triebel S., Reinke H., Tschesche H.;
RT "Formation of a covalent Hg-Cys-bond during mercurial activation of
RT PMN procollagenase gives evidence of a cysteine-switch mechanism.";
RL FEBS Lett. 313:59-61(1992).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
RX MEDLINE=94185631; PubMed=8137810;
RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
RT "The X-ray crystal structure of the catalytic domain of human
RT neutrophil collagenase inhibited by a substrate analogue reveals the
RT essentials for catalysis and specificity.";
RL EMBO J. 13:1263-1269(1994).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
RX MEDLINE=94139300; PubMed=8307185; DOI=10.1016/0014-5793(94)80370-6;
RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
RT Tschesche H., Bode W.;
RT "Structural implications for the role of the N terminus in the
RT 'superactivation' of collagenases. A crystallographic study.";
RL FEBS Lett. 338:227-233(1994).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
RX MEDLINE=95384762; PubMed=7656015;
RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
RA Oronfieh M.W., Banks T.M., Rubin B.;
RT "Structure of human neutrophil collagenase reveals large S1'
RT specificity pocket.";
RL Nat. Struct. Biol. 1:119-123(1994).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
RX MEDLINE=97390108; PubMed=9249047;
RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
RA Bode W., Gomis-Ruth F.-X.;
RT "1.8-A crystal structure of the catalytic domain of human neutrophil
RT collagenase (matrix metalloproteinase-8) complexed with a
RT peptidomimetic hydroxamate primed-side inhibitor with a distinct
RT selectivity profile.";
RL Eur. J. Biochem. 247:356-363(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
RX MEDLINE=98318039; PubMed=9655333;
RA Brandstetter H., Eng R.A., von Roeder E.G., Moroder L., Huber R.,
RA Bode W., Grams F.;

RT "Structure of malonic acid-based inhibitors bound to human neutrophil
RT collagenase. A new binding mode explains apparently anomalous data.";
RL Protein Sci. 7:1303-1309(1998).
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
CC type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
CC -!- ENZYME REGULATION: Cannot be activated without removal of the
CC activation peptide.
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- TISSUE SPECIFICITY: Neutrophils.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; J05556; AAA88021.1; -.
DR PIR; A37073; KCHUN.
DR PDB; 1A85; X-ray; A=105-262.
DR PDB; 1A86; X-ray; A=105-262.
DR PDB; 1B25; X-ray; A=99-263.
DR PDB; 1I73; X-ray; A=100-262.
DR PDB; 1I76; X-ray; A=100-262.
DR PDB; 1JAN; X-ray; A=99-262.
DR PDB; 1JAO; X-ray; A=100-262.
DR PDB; 1JAP; X-ray; A=100-262.
DR PDB; 1JAH; X-ray; A=105-262.
DR PDB; 1JH1; X-ray; A=105-262.
DR PDB; 1JH9; X-ray; A=100-262.
DR PDB; 1KBC; X-ray; A/B=99-262.
DR PDB; 1MNB; X-ray; @=100-262.
DR PDB; 1MNC; X-ray; @=101-263.
DR MEROPS; M10.002; -.
DR Genew; HGNC:7175; MMP8.
DR MIM; 120355; -.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0008130; F:neutrophil collagenase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0008508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW 3D-structure; Calcium-binding; Collagen degradation;
KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 20
FT PROPEP 21 100 Activation peptide.
FT CHAIN 101 467 Neutrophil collagenase.
FT DOMAIN 276 467 Hemopexin-like.
FT SITE 91 91 Cysteine switch.
FT METAL 157 157 Calcium 1.
FT METAL 167 167 Zinc 1.
FT METAL 169 169 Zinc 1.
FT METAL 174 174 Calcium 2.
FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
FT METAL 182 182 Zinc 1.

RA Balbin M., Fueyo A., Knauper V., Lopez J.M., Alvarez J., Sanchez L.M.,
RA Quesada V., Bordallo J., Murphy G., Lopez-Otin C.,
RT "Identification and enzymatic characterization of two diverging murine
RT counterparts of human interstitial collagenase (MMP-1) expressed at
RT sites of embryo implantation.";
RL J. Biol. Chem. 276:10253-10262(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Whole body;
RX STRAIN=C57BL/6J; TISSUE=Whole body;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SvJ;
RA Brathwaite M., Waeltz P., Negaraja R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ278462; CAC18880.1; -.
DR EMBL; AK049552; BAC33807.1; -.

DR EMBL; AY211543; AAO37582.1; -.
DR HSSP; P08254; 1H7.
DR MEROPS; M10.033; -.
DR MGD; MGI:1933846; Mmpla.
DR GO; GO:0008133; F:collagenase activity; IDA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMc; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Collagen.
SQ SEQUENCE 464 AA; 53488 MW; 09PFC04705F59948 CRC64;

Query Match 69.9%; Score 204; DB 2; Length 464;
Best Local Similarity 66.7%; Pred.No. 9.7e-18;
Matches 36; Conservative 6; Mismatches 12; Indels 0; Gaps 0;

QY 1 MOEFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLTYYRIEN 54
DB 64 MQQLGLKVTGNSDFETLRANKRPGVDPDVAFYATHNNPRWTKHLYTSLN 117

RESULT 11
MM08 RAT STANDARD; PRT; 466 AA.
ID MM08 RAT
AC 088766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowne D., Wells G., Burel S., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of
RT rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
CC type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Cannot be activated without removal of the
CC activation peptide (by similarity).
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC -----
DR EMBL; AJ007286; CAA07432.1; -.
DR HSSP; P22894; 1BZS.

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DR MEROPS; M10.002; --
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin_4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRXIN.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolyase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 178 178 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By similarity).
FT METAL 183 183 Zinc 1 (By similarity).
FT METAL 190 190 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 192 192 Calcium 1 (via carbonyl oxygen) (By similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 379 379 Calcium 3 (via carbonyl oxygen) (By similarity).
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By similarity).
FT DISULFID 280 465 Probable.
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;

Query Match 67.1%; Score 196; DB 1; Length 466;
Best Local Similarity 63.0%; Pred. No. 1.1e-16;
Matches 34; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 MQEFGKVTGKPDATLKVMPKPCGVPDVAQVLTGKPNRWEQTHLYRIEN 54
DB 67 MQRFVGLPFGKPDATIEIMKPCGVPDSDGDFLLTPGSKWTHNLTYRIIN 120

RESULT 12
MM10_HUMAN
ID MM10_HUMAN STANDARD; PRT; 476 AA.
AC F09238;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-2 precursor (EC 3.4.24.22) (Matrix metalloproteinase-10)
GN (MMP-10) (Transin-2) (SL-2).
Name=MMP10; Synonyms=STMY2;

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88339885; PubMed=2844164;
RA Muller D., Quantin B., Gesnel M.-C., Millon-Collard R., Abecassis J.,
RA Breathnach R.;
RT "The collagenase gene family in humans consists of at least four
RT members.";
RL Biochem. J. 253:187-192(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.
RA Klausner R.D., Collins F.S., Wagner L., Stenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Whiting M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: Can degrade fibronectin, gelatins of type I, III, IV,
CC and V; weakly collagens III, IV, and V. Activates procollagenase.
CC -1- CATALYTIC ACTIVITY: Similar to stromelysin 1, but action on
CC collagen types III, IV and V is weak.
CC -1- COFACTOR: Binds 2 zinc ions per subunit, calcium (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
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CC -----
DR EMBL; X07820; CAA30679.1; --
DR EMBL; BC002591; AAH02591.1; --
DR PIR; A28816; KCHUS2.
DR HSP; P08254; IG05.
DR MEROPS; M10.006; --
DR Genew; HGNC:7156; MMP10.
DR H-InvDB; HIX0010066; --
DR MIM; 185260; --
DR GO; GO:0005578; C:extracellular matrix; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0004222; F:metalloendopeptidase activity; TAS.
DR GO; GO:0008270; F:zinc ion binding; TAS.
DR GO; GO:0005508; P:proteolysis and peptidolysis; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept M10A_M12B.
DR InterPro; IPR006025; Pept M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase_M10; 1.
DR Pfam; PF09333; Peptidase_M10_N; 1.

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DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; Zmc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium; Collagen degradation; Extracellular matrix; Hydrolase;
KW Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 17 Probable.
FT PROPEP 18 98 Activation peptide.
FT CHAIN 99 476 Stromelysin-2.
FT DOMAIN 286 476 Hemopexin-like.
FT SITE 91 91 Cysteine switch (By similarity).
FT METAL 217 217 Zinc (catalytic) (By similarity).
FT ACT_SITE 218 218 By similarity.
FT METAL 221 221 Zinc (catalytic) (By similarity).
FT METAL 227 227 Zinc (catalytic) (By similarity).
FT DISULFID 289 476 By similarity.
SQ SEQUENCE 476 AA; 54151 MW; 516DCDDPEF92A0D6 CRC64;

Query Match 64.7%; Score 189; DB 1; Length 476;
Best Local Similarity 63.0%; Pred.No. 8.8e-16;
Matches 34; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MQEFGKLVKTPDAETLKMVKPGCVDPVQAFVLTEGNGPRWEQTHLYRIEN 54
Db 66 MQKFLGLEVTGKLDITLWVKRPGCVDPVGHFSPGMPKWKTHLYRIWN 119

RESULT 13
MM03 HUMAN
ID MM03 HUMAN STANDARD; PRT; 477 AA.
AC P08254;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
DE (MMP-3) (Transin-1) (SL-1).
GN Name=MMP3; Synonyms=STMX1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
RX MEDLINE=88198243; PubMed=3350803;
RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
RA Kurkinen M.;
RT "The complete primary structure of human matrix metalloproteinase-3.
RT Identity with stromelysin.";
RL J. Biol. Chem. 263:6742-6745(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Fibroblast;
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
RT "Comparison of human stromelysin and collagenase by cloning and
RT sequence analysis.";
RL Biochem. J. 240:913-916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88016164; PubMed=3477804;
RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marmer B.L.,
RA Grant G.A., Bauer E.A., Goldberg G.I.;
RT "Human skin fibroblast stromelysin: structure, glycosylation,
RT substrate specificity, and differential expression in normal and
RT tumorigenic cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:6725-6729(1987).
RN [4]
RP SEQUENCE FROM N.A.
RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
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RA Kurdi O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
RA Heller R., Davis R.W.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT GLU-45.
RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA Nickerson D.A.;
RT "SeattlesNP. NHLBI HL66682 program for genomic applications, UW-
RT PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP ZYMOGEN ACTIVATION.
RX MEDLINE=90344802; PubMed=2383557;
RA Nagase H., Engchild J.J., Suzuki K., Salvesen G.;
RT "Stepwise activation mechanisms of the precursor of matrix
RT metalloproteinase 3 (stromelysin) by proteinases and (4-
RT aminophenyl)mercuric acetate.";
RL Biochemistry 29:5783-5789(1990).
RN [7]
RP STRUCTURE BY NMR OF CATALYTIC DOMAIN.
RX MEDLINE=95384761; PubMed=7656014;
RA Cooley P.R., O'Connell J.F., Marcy A.I., Cuca G.C., Salowe S.P.,
RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
RA Johnson B.A.;
RT "The NMR structure of the inhibited catalytic domain of human
RT stromelysin-1.";
RL Nat. Struct. Biol. 1:111-118(1994).
RN [8]
RP STRUCTURE BY NMR OF 100-267.
RX MEDLINE=99043696; PubMed=9827994;
RA Stockman B.J., Waldon D.J., Gates J.A., Scahill T.A.,
RA Kloosterman D.A., Mizzak S.A., Jacobsen E.J., Belonga K.L.,
RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
RA Ledbetter S.R., Kaytes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
RA Poorman R.A.;
RT "Solution structures of stromelysin complexed to thiadiazole
RT inhibitors.";
RL Protein Sci. 7:2281-2286(1998).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
RX MEDLINE=96117647; PubMed=8535233;
RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,
RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
RA Hermes J.D., Springer J.P.;
RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
RT domain and of the C-truncated proenzyme.";
RL Protein Sci. 4:1966-1976(1995).
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266.
RX MEDLINE=96311273; PubMed=8740360; DOI=10.1016/S0969-2126(96)00043-3;
RA Dhanraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.P.,
RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
RT "X-ray structure of a hydroxamate inhibitor complex of stromelysin
RT catalytic domain and its comparison with members of the zinc
RT metalloproteinase superfamily.";
RL Structure 4:375-386(1996).
RN [11]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
RX MEDLINE=97236965; PubMed=9083493; DOI=10.1021/jm960465t;
RA Girotra N.N., Kopka I.E., Lanza T.J., Levorse D.A., Maccoss M.,
RA Owens K.A., Ponpipom M.M., Simeone J.P., Harrison R.K.,
RA Niedzwiecki L., Becker J.W., Marcy A.I., Axel M.G., Christen A.J.,
RA McDonnell J., Moore V.L., Olszewski J.M., Saphos C., Visco D.M.,
RA Shen F., Colletti A., Krieter P.A., Hagmann W.K.;
RT "Inhibition of stromelysin-1 (MMP-3) by p1'-biphenylylethyl
RT carboxyalkyl dipeptides.";
RL J. Med. Chem. 40:1026-1040(1997).
RN [12]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 100-267 IN COMPLEX WITH
RP TIMP1.
RX MEDLINE=97433330; PubMed=9288970; DOI=10.1038/37995;
RA Gomis-Rueth F.-X., Maskos K., Betz M., Bergner A., Huber R.,
```

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DR PDB; 1D8F; X-ray; A/B=100-272.
DR PDB; 1D8M; X-ray; A/B=100-272.
DR PDB; 1G05; X-ray; A/B=100-272.
DR PDB; 1G49; X-ray; A/B=100-272.
DR PDB; 1G4K; X-ray; A/B=C=100-267.
DR PDB; 1HFS; X-ray; @=105-264.
DR PDB; 1HW7; X-ray; A/B=100-272.
DR PDB; 1HWI; X-ray; A/B=100-268.
DR PDB; 1LW7; Model; A=100-268.
DR PDB; 1O09; NMR; A=100-267.
DR PDB; 1QIA; X-ray; A/B/C/D=106-267.
DR PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR PDB; 1SLM; X-ray; @=18-272.

Query Match      64.7%; Score 189; DB 1; Length 477;
Best Local Similarity 63.0%; Pred.No. 8.8e-16;
Matches 34; Conservative          9; Mismatches 11; Indels 0; Gaps 0;

Qy   1 MQEFFGLKVTGKPDASTLKVMKPCRGVDPVAQFVLTEGNPRVEQTHLTYYRIEN 54
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Db   67 MQKFLELVGTGVKDSDTLEVWRKPCRGPVDVGHFRTFFPGIPKWKTKHTLYRIN 120

RESULT 14
Q6Y4Q5 PRELIMINARY; PRT; 478 AA.
ID Q6Y4Q5 AC Q6Y4Q5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Names=WMF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Garcoma;
RA Rosensen K.C., Balkin R.G., Ktichell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
RE EMBL; AV183143; AAC63580.1; -.
DR HSSP; P08254; IBD3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR009070; PGSD like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMc; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;

Query Match      64.7%; Score 189; DB 2; Length 478;
Best Local Similarity 61.1%; Pred.No. 8.8e-16;
Matches 33; Conservative          9; Mismatches 12; Indels 0; Gaps 0;

Qy   1 MQEFFGLKVTGKPDASTLKVMKPCRGVDPVAQFVLTEGNPRVEQTHLTYYRIEN 54
    ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db   67 MQKFLELVGTGVKDSDTLAMRRPCRGPVDVGDFTTFFPGMPKWKTKHTLYRIN 120

RESULT 15
Q9N283 PRELIMINARY; PRT; 145 AA.
ID Q9N283 AC Q9N283
AC Q9N283
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DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE MWP-3 (Fragment).
 GN Name=bmp-3;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sato T., Hirata M., Ito A., Hashizume K.;
 RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB043995; BAA96388.1; -.
 DR HSSP; P08254; IQIA.
 DR MEROPS; M10.006; -.
 DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
 DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
 DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR009070; PGHD_like.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRIXIN.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; UNKNOWN_1.
 FT NON_TER 145
 SQ SEQUENCE 145 AA; 16673 MW; 6DFAB43B733579E2 CRC64;

Query Match 63.7%; Score 186; DB 2; Length 145;
 Best Local Similarity 59.3%; Pred. No. 6e-16;
 Matches 32; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

OY 1 MQEFGGLKVTGKPAETLKYMKQPRCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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 Db 67 MQKFLGLEVTGKLDSDTLVIRKPRCGIPDVGFSTFGSPKWKTKHLYRIYN 120

Search completed: May 27, 2005, 06:57:32
 Job time : 95.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 104.885 seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

Sequence: 1 MQEFLKVGKTPDAETLVK.....VLTEGPNRWEQTHLYRIEN 54

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	292	100.0	54	6	ABP97131 Human mat
2	292	100.0	54	6	ABG76317 Human mat
3	292	100.0	54	8	ADQ17092 Human mat
4	292	100.0	454	7	ADE16002 G-coupled
5	292	100.0	454	7	ADE16004 G-coupled
6	292	100.0	454	7	ADE16008 G-coupled
7	292	100.0	454	7	ADE16006 G-coupled
8	292	100.0	454	8	ADL93945 Human G-c
9	292	100.0	454	8	ADL93943 Human G-c
10	292	100.0	455	8	ADL93941 Human G-c
11	292	100.0	469	4	AAB84606 Amino aci
12	292	100.0	469	4	AAE10415 Human mat
13	292	100.0	469	6	ABU03466 Angiogene
14	292	100.0	469	6	ABR58543 Human can
15	292	100.0	469	6	ABR58542 Human can
16	292	100.0	469	6	ABR48148 Human bla
17	292	100.0	469	6	ABU56596 Lung canc
18	292	100.0	469	6	ABU56597 Lung canc
19	292	100.0	469	6	ABU07454 Protein d
20	292	100.0	469	6	ABP54454 Matrix me
21	292	100.0	469	7	ADB79176 Matrix me
22	292	100.0	469	7	ADE34550 Human ski
23	292	100.0	469	7	ADE16000 G-coupled
24	292	100.0	469	7	ADE16010 G-coupled
25	292	100.0	469	7	ADN39849 Cancer/an

ALIGNMENTS

RESULT 1

ABP97131
ID ABP97131 standard; peptide; 54 AA.

XX AC ABP97131;

DT XX 24-JUN-2003 (first entry)

DE DE Human matrix metalloproteinase 1 cleavage region peptide SEQ ID NO:9.

XX KW Human; matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.
XX OS Homo sapiens.

PN WO2003018748-A2.

PD 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

PR 21-DEC-2001; 2001US-00032376.

PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Weart IF;

XX WPI; 2003-381408/36.

XX Anti-angiogenic composition comprising peptide inhibitor of matrix metalloproteinase, useful for decreasing the expression of vascular endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

CC The present invention describes an anti-angiogenic composition (I) for inhibiting expression of vascular endothelial growth factor (VEGF). (I) comprises an effective amount of a peptide inhibitor of matrix metalloproteinase (MMP), where the peptide can inhibit the expression of VEGF. (I) has cytostatic, vulnary, cardiant, cerebroprotective, antidiabetic, ophthalmological activities. (I) can be

Adn38694 Cancer/an
Adn38696 Cancer/an
Adn38698 Cancer/an
Adn38699 Human BEC
Adn38700 Human G-c
Adn38701 Human col
Adn38702 Human col
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Adn39000 Human col

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (1) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (1) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;
 Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||

RESULT 2
 ABG76317
 ID ABG76317 standard; protein; 54 AA.
 AC ABG76317;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #9.
 XX
 KW Human; peptide inhibitor; matrix metalloproteinase-1; MMP-1;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.
 XX
 OS Homo sapiens.

XX
 PN WO2003016520-A1.
 XX
 PD 27-FEB-2003.
 XX
 PF 15-AUG-2002; 2002WO-US026198.
 XX
 PR 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

XX Quirk S, Malik S, Villanueva JM;
 XX WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating wounds, preventing scarring, improving skin tone,
 CC reducing wrinkling and for stimulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs
 XX

SQ Sequence 54 AA;

Query Match 100.0%; Score 292; DB 6; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||

RESULT 3
 ADQ17092
 ID ADQ17092 standard; peptide; 54 AA.
 AC ADQ17092;
 XX

DT 23-SEP-2004 (first entry)

XX Human matrix metalloproteinase-1 (MMP1) cleavage region peptide.
 DE Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.

XX Homo sapiens.

OS US2004127421-A1.

PN 01-JUL-2004.

XX 30-DEC-2002; 2002US-00335207.

XX 30-DEC-2002; 2002US-00335207.

XX (MALI/) MALIK S.

XX (QUIR/) QUIRK S.

XX Malik S, Quirk S;

XX WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.

XX Example 1; SEQ ID NO 9; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 54 AA;

Query Match 100.0%; Score 292; DB 8; Length 54;

Best Local Similarity 100.0%; Pred. No. 1.4e-32;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||
 Db 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 |||||

RESULT 4

AD16002

ID ADE16002 standard; protein; 454 AA.

XX ADE16002;

XX 29-JAN-2004 (first entry)

DE G-coupled protein receptor related polypeptide, SEQ ID No 32.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
OS
OS Homo sapiens.
XX
PN WO200283841-A2.
XX
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282934P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 19-APR-2001; 2001US-0285609P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 23-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286088P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voas EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak K, Fatturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
XX WPI; 2003-067574/06.
XX N-PSDB; ADE16001.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 32; 320pp; English.
XX
XX The invention relates to a novel isolated G-coupled protein receptor
XX related polypeptides. The novel polypeptide comprise any of the 22 fully
XX defined sequences of 87-1780 amino acids, given in the specification;
XX their mature forms; and possible variants. The novel polypeptides have
XX the following activities: antidiabetic, anorectic, antibacterial,
XX virucide, fungicide, cytostatic, neurotropic, neuroprotective,
XX antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
XX receptor related polypeptides are useful in a method of treating or
XX preventing in a human, a pathology associated with the G-coupled protein
XX receptor related polypeptides. The polypeptides are useful in the
XX manufacture of a medicament for treating a syndrome associated with a
XX human disease, preferably a NOVX-associated disorder. The novel
XX polypeptides are useful for treating, preventing or diagnosing diseases,
XX such as metabolic disorders, diabetes, obesity, infectious diseases,
XX anorexia, cancer-associated diseases, neurodegenerative disorders,
XX

CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
XX Sequence 454 AA;
XX

Query Match 100.0%; Score 292; DB 7; Length 454;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQEFFGLKVTGKPDATLKVWKQPRCGVDPVQAQFVLTEGPRWQTHLYRIEN 54
Db 50 MQEFFGLKVTGKPDATLKVWKQPRCGVDPVQAQFVLTEGPRWQTHLYRIEN 103

RESULT 5
ADE16004
ID ADE16004 standard; protein; 454 AA.
XX
AC ADE16004;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID No 34.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
XX WO200283841-A2.
XX
XX 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX
XX 03-APR-2001; 2001US-0281136P.
XX 05-APR-2001; 2001US-0281863P.
XX 10-APR-2001; 2001US-0281906P.
XX 13-APR-2001; 2001US-0282934P.
XX 13-APR-2001; 2001US-0283657P.
XX 13-APR-2001; 2001US-0283678P.
XX 13-APR-2001; 2001US-0283710P.
XX 17-APR-2001; 2001US-0284234P.
XX 19-APR-2001; 2001US-0285325P.
XX 20-APR-2001; 2001US-0285609P.
XX 23-APR-2001; 2001US-0285748P.
XX 24-APR-2001; 2001US-0286088P.
XX 27-APR-2001; 2001US-0287213P.
XX 03-MAY-2001; 2001US-0288509P.
XX 31-MAY-2001; 2001US-0294801P.
XX 31-JUL-2001; 2001US-0309216P.
XX 25-SEP-2001; 2001US-0324775P.
XX 28-NOV-2001; 2001US-0333900P.
XX 02-APR-2002; 2002US-00115479.
XX

PA (CURA-) CURAGEN CORP.
 XX
 PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Raetelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 DR WPI; 2003-067574/06.
 DR N-PSDB; ADE16003.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 PS Claim 1; SEQ ID NO 34; 320pp; English.
 XX
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeimic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX
 SQ Sequence 454 AA;
 Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MOEFFGLKVTGKPDARTLKWMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
 DB 50 MOEFFGLKVTGKPDARTLKWMPKPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103
 RESULT 6
 ID ADE16008
 ID ADE16008 standard; protein; 454 AA.
 AC ADE16008;
 XX
 XX 29-JAN-2004 (first entry)
 DT
 DE G-coupled protein receptor related polypeptide, SEQ ID NO 38.
 XX
 XX G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipaeimic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

KW preventive medicine; pharmacogenomics; human.
 XX
 OS Homo sapiens.
 XX
 PN WO200283841-A2.
 PN
 PD 24-OCT-2002.
 XX
 XX 03-APR-2002; 2002WO-US010713.
 XX
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX
 XX (CURA-) CURAGEN CORP.
 XX
 PA Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Raetelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX
 XX WPI; 2003-067574/06.
 XX N-PSDB; ADE16007.
 XX
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX
 XX Claim 1; SEQ ID NO 38; 320pp; English.
 PS
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipaeimic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidaemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

XX
 SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54
 |||||
 Db 50 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

RESULT 7

ADE16006

ID ADE16006 standard; protein; 454 AA.

XX

AC ADE16006;

XX

DT 29-JAN-2004 (first entry)

XX

DE G-coupled protein receptor related polypeptide, SEQ ID No 36.

XX

KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;

KW virucide; fungicide; cytostatic; nootropic; neuroprotective;

KW antiparkinsonian; haemostatic; antilipaeamic; neurogenesis;

KW cell differentiation; cell proliferation; hematopoiesis; wound healing;

KW angiogenesis; gene therapy; chromosome mapping; tissue typing;

KW preventive medicine; pharmacogenomics; human.

XX Homo sapiens.

OS

XX WO200283841-A2.

XX

XX 24-OCT-2002.

XX

XX 03-APR-2002; 2002WO-US010713.

XX

XX 03-APR-2001; 2001US-0281136P.

XX

XX 05-APR-2001; 2001US-0281863P.

XX

XX 05-APR-2001; 2001US-0281906P.

XX

XX 10-APR-2001; 2001US-0282934P.

XX

XX 13-APR-2001; 2001US-0283657P.

XX

XX 13-APR-2001; 2001US-0283678P.

XX

XX 13-APR-2001; 2001US-0283687P.

XX

XX 13-APR-2001; 2001US-0283710P.

XX

XX 17-APR-2001; 2001US-0284234P.

XX

XX 19-APR-2001; 2001US-0285325P.

XX

XX 20-APR-2001; 2001US-0285609P.

XX

XX 23-APR-2001; 2001US-0285748P.

XX

XX 23-APR-2001; 2001US-0285890P.

XX

XX 24-APR-2001; 2001US-0286068P.

XX

XX 27-APR-2001; 2001US-0287213P.

XX

XX 03-MAY-2001; 2001US-0288509P.

XX

XX 30-MAY-2001; 2001US-0294495P.

XX

XX 31-MAY-2001; 2001US-0294801P.

XX

XX 31-JUL-2001; 2001US-0309216P.

XX

XX 28-SEP-2001; 2001US-0324775P.

XX

XX 28-NOV-2001; 2001US-0333900P.

XX

XX 02-APR-2002; 2002US-00115479.

XX

XX (CURA-) CURAGEN CORP.

XX

XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;

XX

XX Pena CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;

XX

XX Voss EZ, Vernet CAM, MacDougall JR, Rastelli L, Anderson DM;

XX

XX Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;

XX

XX Shimkets RA, Taupier RJ, Edinger SR, Mazur A;

XX

XX

DR WPI; 2003-067574/06.

XX

XX N-PSDB; ADE16005.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOVX-associated disorders e.g.

PT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,

PT Alzheimer's disease, infections.

XX

XX Claim 1; SEQ ID NO 36; 320pp; English.

XX

XX The invention relates to a novel isolated G-coupled protein receptor

XX related polypeptides. The novel polypeptide comprise any of the 22 fully

XX defined sequences of 87-1780 amino acids, given in the specification;

XX their mature forms; and possible variants. The novel polypeptides have

XX the following activities: antidiabetic, anorectic, antibacterial,

XX virucide, fungicide, cytostatic, nootropic, neuroprotective,

XX antiparkinsonian, haemostatic, and antilipaeamic. The G-coupled protein

XX receptor related polypeptides are useful in a method of treating or

XX preventing in a human, a pathology associated with the G-coupled protein

XX receptor related polypeptides. The polypeptides are useful in the

XX manufacture of a medicament for treating a syndrome associated with a

XX human disease, preferably a NOVX-associated disorder. The novel

XX polypeptides are useful for treating, preventing or diagnosing diseases,

XX such as metabolic disorders, diabetes, obesity, infectious diseases,

XX anorexia, cancer-associated diseases, neurodegenerative disorders,

XX Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic

XX disorders, and various dyslipidaemias, metabolic disturbances associated

XX with obesity, metabolic X syndrome and wasting disorders associated with

XX chronic diseases and various cancers. The nucleic acids and polypeptides

XX may also be used as targets for the identification of small molecules

XX that modulate or inhibit e.g. neurogenesis, cell differentiation, cell

XX proliferation, hematopoiesis, wound healing and angiogenesis, in gene

XX therapy, in generation of antibodies that bind immunospecifically to NOVX

XX substances for use in therapeutic or diagnostic methods. The nucleic

XX acids are further used as hybridization probes, in chromosome mapping,

XX tissue typing, preventive medicine, and pharmacogenomics. This sequence

XX represents one of the novel G-coupled protein receptor related

XX polypeptides of the invention.

XX

SQ Sequence 454 AA;

Query Match 100.0%; Score 292; DB 7; Length 454;

Best Local Similarity 100.0%; Pred. No. 2.1e-31;

Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 54

|||||

Db 50 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPRWEQTHLYRIEN 103

|||||

RESULT 8

ADL93945

ID ADL93945 standard; protein; 454 AA.

XX

AC ADL93945;

XX

DT 20-MAY-2004 (first entry)

XX

XX Human G-coupled protein receptor-related protein #18.

XX

XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;

XX atherosclerosis; hypertension; congenital heart defect; aortic stenosis;

XX atrial septal defect; atrioventricular canal defect; ductus arteriosus;

XX pulmonary stenosis; subaortic stenosis; ventricular septal defect;

XX valve disease; tuberosus sclerosis; scleroderma; obesity; transplantation;

XX adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;

XX neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;

XX haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;

XX immunodeficiency; graft versus host disease; AIDS; bronchial asthma;

XX Crohn's disease; G-coupled protein receptor; metabolic disorder;

XX neurodegenerative disorder; receptor.

XX

OS Homo sapiens.
 XX US2004006205-A1.
 PN 08-JAN-2004.
 PD 02-APR-2002; 2002US-00115479.
 PF 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-028378P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285909P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 XX (LILL/) LI L.
 PA (GERL/) GERLACH V.
 PA (LIUX/) LIU X.
 PA (MILL/) MILLER C E.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PENA/) PENNA C E A.
 PA (SHEN/) SHENOY S G.
 PA (ZHON/) ZHONG H.
 PA (SMIT/) SMITHSON G.
 PA (CASW/) CASMAN S J.
 PA (BOLD/) BOLDOW F L.
 PA (VOSS/) VOSS E Z.
 PA (VERN/) VERNET C A.
 PA (MACD/) MACDOUGALL J R.
 PA (RAST/) RASTELLI L.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (MEZE/) MEZES P S.
 PA (FURT/) FURTAK K.
 PA (PATT/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (MALY/) MALYANKAR U M.
 PA (SHIM/) SHIMKETS R A.
 PA (TAUP/) TAUPIER R J.
 PA (EDIN/) EDINGER S.
 PA (MAZU/) MAZUR A.
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Penna CE, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;
 PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;
 XX WPI; 2004-224146/21.
 DR N-PSDB; ADL93944.
 XX New G-coupled protein-receptor related polypeptides, for preventing
 PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
 PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
 PT scleroderma or obesity.
 XX Claim 1; Page 68; 220pp; English.

XX The invention relates to isolated human G-coupled protein receptor-
 CC related polypeptides and polynucleotides. The proteins are useful for
 CC preventing, treating or ameliorating medical disorders by protein or gene
 CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
 CC congenital heart defects, aortic stenosis, atrial septal defect,
 CC atrioventricular canal defect, ductus arteriosus, pulmonary stenosis,
 CC subaortic stenosis, ventricular septal defect, valve diseases, tubercous
 CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
 CC congenital adrenal hyperplasia, prostate cancer, fertility, neoplasm,
 CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
 CC hypercoagulation, idiopathic thrombocytopenic purpura,
 CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
 CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
 CC are also useful as diagnostic or research tools. The present sequence
 CC represents a human G-coupled protein receptor-related protein of the
 CC invention.
 XX
 SQ Sequence 454 AA;
 Query Match 100.0%; Score 292; DB 8; Length 454;
 Best Local Similarity 100.0%; Pred. No. 2.1e-31;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQEFFGLKVTGKPDATLKVMPKQRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 54
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 50 MQEFFGLKVTGKPDATLKVMPKQRCGVDPDVAQFVLTEGNPRWEQTHLYRIEN 103
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 9
 ADL93943
 ID ADL93943 standard; protein; 454 AA.
 XX
 AC ADL93943;
 XX
 DT 20-MAY-2004 (first entry)
 DE Human G-coupled protein receptor-related protein #17.
 XX human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
 KW valve disease; tubercous sclerosis; scleroderma; obesity; transplantation;
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
 KW neurodegenerative disorder; receptor.
 XX Homo sapiens.
 OS
 XX US2004006205-A1.
 PN
 XX 08-JAN-2004.
 PD
 PF 02-APR-2002; 2002US-00115479.
 XX
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-028378P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285909P.
 PR 24-APR-2001; 2001US-0286068P.

PA (MACD/) MACDOUGALL J R.
PA (RAST/) RASTELLI L.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (MEZE/) MEZES P S.
PA (FURT/) FURTA K.
PA (PATT/) PATTURAJAN M.
PA (BURG/) BURGESS C E.
PA (MALY/) MALYANKAR U M.
PA (SHIM/) SHIMKETS R A.
PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernet CA, Macdougall JR, Rastelli L, Anderson DW, Zhong M;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shimkets RA, Taupier RJ, Edinger S, Mazur A;
XX
DR WPI; 2004-224146/21.
DR N-PSDB; ADL93940.
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
PS Claim 1; Page 67; 220pp; English.
XX
XX The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, atrial septal defect,
CC subventricular canal defect, ductus arteriosus, pulmonary stenosis,
CC aortic stenosis, ventricular septal defect, valve diseases, tuberosus
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, neoplasm,
CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
SQ Sequence 455 AA;
Query Match 100.0%; Score 292; DB 8; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
DB 50 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 103
|||||
RESULT 11
AAB84606
ID AAB84606 standard; protein; 469 AA.
XX
XX AAB84606;
AC
XX 05-SEP-2001 (first entry)
DT
XX Amino acid sequence of matrix metalloproteinase collagenase 1.
DE
XX
XX Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
XX
KW (MACD/) MACDOUGALL J R.
KW (RAST/) RASTELLI L.
KW (ANDE/) ANDERSON D W.
KW (ZHON/) ZHONG M.
KW (MEZE/) MEZES P S.
KW (FURT/) FURTA K.
KW (PATT/) PATTURAJAN M.
KW (BURG/) BURGESS C E.
KW (MALY/) MALYANKAR U M.
KW (SHIM/) SHIMKETS R A.
KW (TAUP/) TAUPIER R J.
KW (EDIN/) EDINGER S.
KW (MAZU/) MAZUR A.
XX
OS Homo sapiens.
XX WO200149309-A2.
PN 12-JUL-2001.
XX
XX 21-DEC-2000; 2000WO-IB001935.
PF 29-DEC-1999; 99GB-00030768.
PR
XX (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
PI Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX WPI; 2001-418351/44.
DR N-PSDB; AAH28221.
XX
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
PT dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
PT factor.
XX
PS Disclosure; Page 551; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
CC growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
CC inhibits the action of at least one specific adverse protein, i.e. a
CC protease, that is upregulated in a damaged tissue such as a wound
CC environment. Growth factors which are included in the composition of the
CC invention are platelet-derived growth factor (PDGF), fibroblast growth
CC factor (FGF), connective tissue derived growth factor (CTGF),
CC keratinocyte-derived growth factor (KGF), transforming growth factor-beta
CC (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
CC epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
CC and chrysalin. Inhibitors which are included in the composition of the
CC invention include inhibitors of urokinase-type plasminogen activator
CC (uPA) and matrix metalloproteinase (MMP). The composition is useful for
CC the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
CC The present sequence represents a human MMP-1, and is used to produce the
CC composition of the invention
XX
SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
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DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120
|||||
RESULT 12
AAE10415
ID AAE10415 standard; protein; 469 AA.
XX
XX AAE10415;
AC
XX 10-DEC-2001 (first entry)
DT
XX Human matrix metalloproteinase-1 (MMP-1) protein.
DE
XX Human; matrix metalloproteinase; MMP-1; hair growth; antisense therapy;
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH Peptide 1..19
FT

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FT Protein /label= Signal_peptide
FT 20..469
FT /label= Mature_MMP_1_protein
FT Domain 90..96
FT /label= Cysteine_switch_domain
FT Domain 161..171
FT /note= "Zinc and calcium binding domain"
XX WO200166766-A2.
XX PN
XX XX
XX 13-SEP-2001.
XX PD
XX PF 06-MAR-2001; 2001WO-US007167.
XX XX
XX PF 06-MAR-2000; 2000US-0187196P.
XX XX
XX (DARW-) DARWIN MOLECULAR CORP.
XX (SCHA/) SCHATZMAN R.
XX PI Fajardo M, Wang K, Smith R, Moss P;
XX XX
XX WPI; 2001-582276/65.
XX DR
XX XX
XX Novel isolated matrix metalloproteinase-25 nucleic acid molecule and
XX PT proteins encoded by them whose inhibition is useful for modulation of
XX PT hair growth in mammals.
XX XX
XX Example 2; Fig 3; 119pp; English.
XX XX
XX The present sequence is human matrix metalloproteinase (MMP)-1 protein
XX CC used in the exemplification of the invention. MMP-25 DNA is located on
XX CC chromosome 11q22. Matrix metalloproteinases are a family of zinc
XX CC dependent endopeptidases that function extracellularly to degrade
XX CC proteins typically found in the extracellular matrix. MMP-25 is expressed
XX CC in skin cells of mammals, particularly in breast cells and hair
XX CC follicles. MMP-25 DNA is useful for identifying a nucleic acid molecule
XX CC encoding all or part of MMP by hybridising MMP-25 to a nucleic acid
XX CC sample and identifying a sequence that hybridises in the nucleic acid
XX CC sample. The identification step involves performing polymerase chain
XX CC reaction (PCR) to amplify the hybridising sequence. MMP-25 antibody is
XX CC useful for identifying type 25 MMP. MMP-25 protein inhibitors may be used
XX CC to modulate hair growth and breast cancer in a mammal
XX SQ Sequence 469 AA;

Query Match 100.0%; Score 292; DB 4; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPRWQTHLTYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPRWQTHLTYRIEN 120

RESULT 13
ABU03466
ID ABU03466 standard; protein; 469 AA.
XX XX
XX AC ABU03466;
XX XX
XX 21-JAN-2003 (first entry)
XX DT
XX DE Angiogenesis-associated human protein sequence #11.
XX XX
XX Human; angiogenesis-associated transcript; angiogenesis;
XX KW angiogenesis-associated disease; cancer; cytostatic.
XX XX
XX Homo sapiens.
XX OS
XX WO200279492-A2.
XX PN
XX 10-OCT-2002.
XX PD
XX XX

14-FEB-2002; 2002WO-US004915.
XX PF
XX 14-FEB-2001; 2001US-00784356.
XX PR
XX 22-FEB-2001; 2001US-00791390.
XX PR
XX 19-APR-2001; 2001US-0285475P.
XX PR
XX 03-AUG-2001; 2001US-0310025P.
XX PR
XX 13-NOV-2001; 2001US-0350666P.
XX PR
XX 29-NOV-2001; 2001US-0334244P.
XX XX
XX (EOSB-) EOS BIOTECHNOLOGY INC.
XX PA
XX Murray R, Glynn R, Watson SR, Aziz N;
XX PI
XX WPI; 2003-040681/03.
XX DR
XX N-PSDB; ABX08749.
XX DR
XX PT Detecting angiogenesis-associated transcript in a cell for diagnosing and
XX PT treating cancer by contacting a sample with a polynucleotide that
XX PT exhibits changes in expression level as a function of time in tissue
XX PT undergoing angiogenesis.
XX FT
XX XX
XX Example 2; Page 189; 291pp; English.
XX PS
XX XX
XX The present invention relates to methods and compositions for detecting
XX CC an angiogenesis-associated transcript in a cell in a patient. The method
XX CC involves contacting a biological sample from the patient with a
XX CC polynucleotide that selectively hybridises to a sequence at least 80%
XX CC identical to any of the angiogenesis-associated human polynucleotide
XX CC sequences given in the specification. These angiogenesis-associated
XX CC polynucleotide sequences comprise genes that exhibit changes in
XX CC expression levels as a function of time in tissue undergoing
XX CC angiogenesis. The method and the polynucleotide sequences of the
XX CC invention are useful for diagnosing and treating angiogenesis and
XX CC angiogenesis-associated diseases e.g. cancer. The polynucleotide
XX CC sequences are also useful in the gene therapy of such disorders. The
XX CC angiogenesis-associated proteins encoded by the polynucleotide sequences
XX CC are useful as a vaccine for therapeutic and prophylactic immunisation.
XX CC ABU03456-ABU03569 represent angiogenesis-associated protein sequences
XX XX
XX SQ Sequence 469 AA;

Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPRWQTHLTYRIEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVPDVAQFVLTEGPRWQTHLTYRIEN 120

RESULT 14
ABR58543
ID ABR58543 standard; protein; 469 AA.
XX XX
XX AC ABR58543;
XX XX
XX 09-JUL-2003 (first entry)
XX DT
XX DE Human cancer related protein SEQ ID NO:200.
XX XX
XX Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
XX KW heart disease; atherosclerosis; endometriosis.
XX XX
XX Homo sapiens.
XX OS
XX WO2003025138-A2.
XX PN
XX 27-MAR-2003.
XX PD
XX 17-SEP-2002; 2002WO-US029560.
XX PF
XX 17-SEP-2001; 2001US-0323469P.
XX PR
XX 20-SEP-2001; 2001US-0323887P.
XX PR

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PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
PA (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72663.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 735; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

RESULT 15
ABR58542
ID ABR58542 standard; protein; 469 AA.
XX
AC ABR58542;
XX
XX 09-JUL-2003 (first entry)
DT
DE Human cancer related protein SEQ ID NO:199.
DE
KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;
KW heart disease; atherosclerosis; endometriosis.
XX
OS Homo sapiens.
XX
XX WO2003025138-A2.
XX
XX 27-MAR-2003.
XX
XX 17-SEP-2002; 2002MO-US029560.
XX
XX 17-SEP-2001; 2001US-0323469P.

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PR 20-SEP-2001; 2001US-0323887P.
PR 13-NOV-2001; 2001US-0350666P.
PR 08-FEB-2002; 2002US-0355145P.
PR 08-FEB-2002; 2002US-0355257P.
PR 12-APR-2002; 2002US-0372246P.
XX
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;
PI Zlotnik A;
XX
XX WPI; 2003-354600/33.
DR N-PSDB; ACC72662.
XX
PT New genes that are up-regulated or down-regulated in cancers, useful as
PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as
PT therapeutic targets for screening drugs for treating these diseases.
XX
PS Claim 12; Page 735; 767pp; English.
XX
CC The present invention describes an isolated nucleic acid molecule, which
CC comprises the sequence of any of the genes that are up-regulated or down-
CC regulated in specific cancers (e.g. about 1031 genes up-regulated in
CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer
CC related gene nucleotide sequences which encode the proteins given in
CC ABR58521 to ABR58709. Also described: (1) determining the presence or
CC absence of a pathological cell in a patient; (2) an expression vector
CC comprising a nucleic acid molecule described above; (3) a host cell
CC comprising the vector; (4) an isolated polypeptide, which is encoded by
CC the nucleic acid; (5) an antibody that specifically binds the polypeptide
CC of (4); (6) specifically targeting a compound to a pathological cell in a
CC patient by administering to the patient the antibody above; and (7) a
CC drug screening assay. The nucleic acid is useful as diagnostic markers or
CC therapeutic targets. In particular, the nucleic acid is useful for
CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,
CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,
CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,
CC atherosclerosis and endometriosis. The nucleic acid is also useful in
CC drug screening, particularly for identifying agents for treating these
CC pathologies
XX
SQ Sequence 469 AA;
Query Match 100.0%; Score 292; DB 6; Length 469;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 54
DB 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGNPRWEQTHLYRIEN 120

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Job time : 106.885 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:53:10 ; Search time 314.308 Seconds
(without alignments)
59.268 Million cell updates/sec

Title: US-10-032-376A-9

Perfect score: 292

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1462099 seqs, 344972447 residues

Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	292	100.0	54	14	US-10-219-561-9
4	292	100.0	54	16	US-10-032-376A-9
5	292	100.0	54	16	US-10-335-207-9
6	292	100.0	454	15	US-10-115-479-32
7	292	100.0	454	15	US-10-115-479-34
8	292	100.0	454	15	US-10-115-479-36
9	292	100.0	454	15	US-10-115-479-38
10	292	100.0	469	9	US-09-391-104-23
11	292	100.0	469	9	US-09-801-196-19
12	292	100.0	469	9	US-09-853-386-100
13	292	100.0	469	14	US-10-301-822-119

14	292	100.0	469	14	US-10-021-660-76	Sequence 76, Appl
15	292	100.0	469	14	US-10-308-279-34	Sequence 34, Appl
16	292	100.0	469	14	US-10-131-985-23	Sequence 23, Appl
17	292	100.0	469	15	US-10-295-027-12	Sequence 12, Appl
18	292	100.0	469	15	US-10-295-027-14	Sequence 14, Appl
19	292	100.0	469	15	US-10-295-027-1167	Sequence 1167, Ap
20	292	100.0	469	15	US-10-295-027-1168	Sequence 1168, Ap
21	292	100.0	469	15	US-10-115-479-30	Sequence 30, Appl
22	292	100.0	469	15	US-10-115-479-40	Sequence 40, Appl
23	292	100.0	469	15	US-10-211-462-22	Sequence 22, Appl
24	292	100.0	469	15	US-10-188-832-6	Sequence 6, Appl
25	292	100.0	469	16	US-10-734-564-109	Sequence 109, App
26	292	100.0	469	17	US-10-901-417-23	Sequence 23, Appl
27	292	100.0	470	15	US-10-447-315-1	Sequence 1, Appl
28	292	100.0	496	14	US-10-106-698-6283	Sequence 6283, Ap
29	233	79.8	43	14	US-10-219-329-17	Sequence 17, Appl
30	233	79.8	43	14	US-10-153-185-17	Sequence 17, Appl
31	233	79.8	43	14	US-10-219-561-17	Sequence 17, Appl
32	233	79.8	43	16	US-10-032-376A-17	Sequence 17, Appl
33	233	79.8	43	16	US-10-335-207-17	Sequence 17, Appl
34	214	73.3	55	14	US-10-219-329-10	Sequence 10, Appl
35	214	73.3	55	14	US-10-153-185-10	Sequence 10, Appl
36	214	73.3	55	14	US-10-219-561-10	Sequence 10, Appl
37	214	73.3	55	16	US-10-032-376A-10	Sequence 10, Appl
38	214	73.3	55	16	US-10-335-207-10	Sequence 10, Appl
39	214	73.3	467	9	US-09-391-104-24	Sequence 24, Appl
40	214	73.3	467	9	US-09-801-196-20	Sequence 20, Appl
41	214	73.3	467	10	US-09-759-1308-176	Sequence 176, App
42	214	73.3	467	14	US-10-131-985-31	Sequence 31, Appl
43	214	73.3	467	16	US-10-741-790-176	Sequence 176, App
44	214	73.3	467	17	US-10-741-600-917	Sequence 917, App
45	214	73.3	467	17	US-10-901-417-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1

US-10-219-329-9

; Sequence 9, Application US/10219329

; Publication No. US20030096757A1

; GENERAL INFORMATION:

; APPLICANT: Quirk, Stephen

; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds

; FILE REFERENCE: 1443.035W01

; CURRENT APPLICATION NUMBER: US/10/219,329

; PRIOR FILING DATE: 2002-08-15

; PRIOR APPLICATION NUMBER: US 10/032,376

; PRIOR FILING DATE: 2001-12-21

; PRIOR APPLICATION NUMBER: US 60/312,726

; PRIOR FILING DATE: 2001-08-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 54

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-219-329-9

Query Match 100.0%; Score 292; DB 14; Length 54;
Best Local Similarity 100.0%; Pred. No. 3.5e-30;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLKVMPKQRCVGPVDAQVLTGPNRWEQTHLYRIEN 54

Db 1 MQEFFGLKVTGKPDATLKVMPKQRCVGPVDAQVLTGPNRWEQTHLYRIEN 54

RESULT 2

US-10-153-185-9

; Sequence 9, Application US/10153185

; Publication No. US20030148959A1

APPLICANT: Burgess, Catherine E.
 APPLICANT: Malyanker, Uriel M.
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Taupier, Raymond J.
 APPLICANT: Edinger, Shlomit R.
 APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 FILE REFERENCE: 21402-322 B (Cura 622 PT)
 CURRENT APPLICATION NUMBER: US/10/115,479
 CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 60/281,136
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/281,863
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/281,906
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/282,934
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 60/283,657
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,678
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,687
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,710
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/284,234
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: 60/285,325
 PRIOR FILING DATE: 2001-04-19

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 198

SEQ ID NO 32

LENGTH: 454

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-479-32

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMKQRCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
 Db 50 MQEFGKLVTKGKDAETLKVMKQRCGVPDVAQFVLTEGPNRWEQTHLYRIEN 103

RESULT 7

US-10-115-479-34
 Sequence 34, Application US/10115479
 Publication No. US20040006205A1
 GENERAL INFORMATION:

APPLICANT: Li, Li
 APPLICANT: Gerlach, Valerie L.
 APPLICANT: Liu, Xiaohong
 APPLICANT: Miller, Charles E.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Zerhusen, Bryan D.
 APPLICANT: Pena, Carol E.A.
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Zhong, Haihong
 APPLICANT: Smithson, Glendda
 APPLICANT: Casman, Stacie J.
 APPLICANT: Boldog, Ferenc L.;
 APPLICANT: Voss, Edward
 APPLICANT: Vernet, Corine
 APPLICANT: MacDougall, John A.
 APPLICANT: Rastelli, Luca
 APPLICANT: Anderson, David W.
 APPLICANT: Zhong, Mei
 APPLICANT: Mezes, Peter S.
 APPLICANT: Furtak, Katarzyna
 APPLICANT: Patturajan, Meera

APPLICANT: Burgess, Catherine E.
 APPLICANT: Malyanker, Uriel M.
 APPLICANT: Shimkets, Richard A.
 APPLICANT: Taupier, Raymond J.
 APPLICANT: Edinger, Shlomit R.
 APPLICANT: Mazur, Ann

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 FILE REFERENCE: 21402-322 B (Cura 622 PT)
 CURRENT APPLICATION NUMBER: US/10/115,479
 CURRENT FILING DATE: 2002-11-18

PRIOR APPLICATION NUMBER: 60/281,136
 PRIOR FILING DATE: 2001-04-03
 PRIOR APPLICATION NUMBER: 60/281,863
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/281,906
 PRIOR FILING DATE: 2001-04-05
 PRIOR APPLICATION NUMBER: 60/282,934
 PRIOR FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 60/283,657
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,678
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,687
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/283,710
 PRIOR FILING DATE: 2001-04-13
 PRIOR APPLICATION NUMBER: 60/284,234
 PRIOR FILING DATE: 2001-04-17
 PRIOR APPLICATION NUMBER: 60/285,325
 PRIOR FILING DATE: 2001-04-19

Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 198

SEQ ID NO 34

LENGTH: 454

TYPE: PRT

ORGANISM: Homo sapiens

US-10-115-479-34

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFGKLVTKGKDAETLKVMKQRCGVPDVAQFVLTEGPNRWEQTHLYRIEN 54
 Db 50 MQEFGKLVTKGKDAETLKVMKQRCGVPDVAQFVLTEGPNRWEQTHLYRIEN 103

RESULT 8

US-10-115-479-36
 Sequence 36, Application US/10115479
 Publication No. US20040006205A1
 GENERAL INFORMATION:

APPLICANT: Li, Li
 APPLICANT: Gerlach, Valerie L.
 APPLICANT: Liu, Xiaohong
 APPLICANT: Miller, Charles E.
 APPLICANT: Spytek, Kimberly A.
 APPLICANT: Zerhusen, Bryan D.
 APPLICANT: Pena, Carol E.A.
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Zhong, Haihong
 APPLICANT: Smithson, Glendda
 APPLICANT: Casman, Stacie J.
 APPLICANT: Boldog, Ferenc L.;
 APPLICANT: Voss, Edward
 APPLICANT: Vernet, Corine
 APPLICANT: MacDougall, John A.
 APPLICANT: Rastelli, Luca
 APPLICANT: Anderson, David W.
 APPLICANT: Zhong, Mei
 APPLICANT: Mezes, Peter S.
 APPLICANT: Furtak, Katarzyna
 APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Malyanker, Uriel M.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)
 ; CURRENT APPLICATION NUMBER: US/10/115,479
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,687
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/285,325
 ; PRIOR FILING DATE: 2001-04-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 198
 ; SEQ ID NO 36
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-115-479-36

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGNGPRWEQHTLYRIEN 54
 DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGNGPRWEQHTLYRIEN 103

RESULT 9
 US-10-115-479-38
 ; Sequence 38, Application US/10115479
 ; Publication No. US20040006205A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Li, Li
 ; APPLICANT: Gerlach, Valerie L.
 ; APPLICANT: Liu, Xiaohong
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Pena, Carol E.A.
 ; APPLICANT: Shency, Suresh G.
 ; APPLICANT: Zhong, Haihong
 ; APPLICANT: Smithson, Glenda
 ; APPLICANT: Casman, Stacie J.
 ; APPLICANT: Boldog, Ferenc L.;
 ; APPLICANT: Voss, Edward
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: MacDougall, John A.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Anderson, David W.
 ; APPLICANT: Zhong, Mei
 ; APPLICANT: Mezes, Peter S.
 ; APPLICANT: Furtak, Katarzyna
 ; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Malyanker, Uriel M.
 ; APPLICANT: Shimkets, Richard A.
 ; APPLICANT: Taupier, Raymond J.
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: Mazur, Ann
 ; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
 ; FILE REFERENCE: 21402-322 B (Cura 622 PT)
 ; CURRENT APPLICATION NUMBER: US/10/115,479
 ; CURRENT FILING DATE: 2002-11-18
 ; PRIOR APPLICATION NUMBER: 60/281,136
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: 60/281,863
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/281,906
 ; PRIOR FILING DATE: 2001-04-05
 ; PRIOR APPLICATION NUMBER: 60/282,934
 ; PRIOR FILING DATE: 2001-04-10
 ; PRIOR APPLICATION NUMBER: 60/283,657
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,678
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,687
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/283,710
 ; PRIOR FILING DATE: 2001-04-13
 ; PRIOR APPLICATION NUMBER: 60/284,234
 ; PRIOR FILING DATE: 2001-04-17
 ; PRIOR APPLICATION NUMBER: 60/285,325
 ; PRIOR FILING DATE: 2001-04-19
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 198
 ; SEQ ID NO 38
 ; LENGTH: 454
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-115-479-38

Query Match 100.0%; Score 292; DB 15; Length 454;
 Best Local Similarity 100.0%; Pred. No. 4e-29;
 Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGNGPRWEQHTLYRIEN 54
 DB 50 MOEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTGNGPRWEQHTLYRIEN 103

RESULT 10
 US-09-391-104-23
 ; Sequence 23, Application US/09391104
 ; Publication No. US20020031817A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Falduto, Michael T.
 ; APPLICANT: Magnuson, Scott R.
 ; APPLICANT: Morgan, Douglas W.
 ; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
 ; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
 ; FILE REFERENCE: 6073.US.P1
 ; CURRENT APPLICATION NUMBER: US/09/391,104
 ; CURRENT FILING DATE: 1999-09-07
 ; PRIOR APPLICATION NUMBER: US 08/814,394
 ; PRIOR FILING DATE: 1997-03-11
 ; NUMBER OF SEQ ID NOS: 35
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-391-104-23

Query Match 100.0%; Score 292; DB 9; Length 469;

Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 11

US-09-801-196-19
; Sequence 19, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moas, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT FILING DATE: 2001-03-06
; CURRENT APPLICATION NUMBER: US/09/801.196
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-19

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 12

US-09-853-386-100
; Sequence 100, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Evelyn
; APPLICANT: Bresnahan, Barry
; APPLICANT: Conneely, Orla
; APPLICANT: Fitzgerald, Oliver
; TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
; FILE REFERENCE: P01972US1
; CURRENT FILING DATE: 2001-05-11
; CURRENT APPLICATION NUMBER: US/09/853.386
; PRIOR FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 100
; LENGTH: 469
; TYPE: PRT
; ORGANISM: HUMAN
US-09-853-386-100

Query Match 100.0%; Score 292; DB 9; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 13

US-10-301-822-119
; Sequence 119, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301.822
; CURRENT FILING DATE: 2002-11-21
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 119
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-301-822-119

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

RESULT 14

US-10-021-660-76
; Sequence 76, Application US/10021660
; Publication No. US20030152926A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Richard
; APPLICANT: Glynn, Richard
; APPLICANT: Watson, Susan R.
; TITLE OF INVENTION: No. US20030152926A1 Methods of Diagnosis of Angiogenesis,
; TITLE OF INVENTION: Compositions and Methods of Screening for Angiogenesis
; FILE REFERENCE: 018501-000710US
; CURRENT APPLICATION NUMBER: US/10/021.660
; CURRENT FILING DATE: 2001-12-06
; PRIOR FILING DATE: 2001-02-14
; PRIOR APPLICATION NUMBER: US 09/784,356
; PRIOR FILING DATE: 2000-08-11
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 76
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-021-660-76

Query Match 100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 54
Db 67 MQEFFGLKVTGKPDATLTKVMKQPCGVPDVAQFVLTEGPNRWEQTHLTTRYEN 120

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Db      67 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTEGNPRWEQTHLTYRIEN 120
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RESULT 15
US-10-308-279-34
; Sequence 34, Application US/10308279
; Publication No. US20030170742A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE DEVELOPMENT
; FILE REFERENCE: D0190 NP
; CURRENT APPLICATION NUMBER: US/10/308,279
; CURRENT FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: 60/337,429
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 469
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-308-279-34

Query Match      100.0%; Score 292; DB 14; Length 469;
Best Local Similarity 100.0%; Pred. No. 4.2e-29;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTEGNPRWEQTHLTYRIEN 54
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Db      67 MQEFFGLKVTGKPDATLKVMPKQPCGVPDVAQFVLTEGNPRWEQTHLTYRIEN 120
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Search completed: May 27, 2005, 07:33:59
Job time : 314.308 secs

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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 26.7949 Seconds
(without alignments)
153.227 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGPKWERTNLTIRNY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	444	1	US-09-178-002-2
2	307	100.0	466	3	US-08-704-711A-17
3	307	100.0	466	3	US-09-521-220-17
4	307	100.0	467	1	US-09-178-002-4
5	307	100.0	467	3	US-09-391-104-24
6	307	100.0	468	3	US-08-448-489-13
7	307	100.0	468	4	US-09-689-730-13
8	221	72.0	469	3	US-08-704-711A-16
9	221	72.0	469	3	US-08-448-489-12
10	221	72.0	469	3	US-09-521-220-16
11	221	72.0	469	3	US-09-391-104-23
12	221	72.0	469	4	US-09-949-016-6223
13	221	72.0	469	4	US-09-689-730-12
14	221	72.0	491	4	US-09-949-016-10875
15	196	63.8	477	3	US-08-704-711A-20
16	196	63.8	477	3	US-08-448-489-15
17	196	63.8	477	3	US-08-281-313-1
18	196	63.8	477	3	US-09-521-220-20
19	196	63.8	477	3	US-09-391-104-21
20	196	63.8	477	4	US-09-689-730-15
21	195	63.5	476	3	US-08-704-711A-21
22	195	63.5	476	3	US-08-448-489-14
23	195	63.5	476	3	US-09-521-220-21
24	195	63.5	476	3	US-09-391-104-22
25	195	63.5	476	4	US-09-949-016-6224
26	195	63.5	476	4	US-09-689-730-14
27	195	63.5	484	4	US-09-949-016-10877

28 188 61.2 471 3 US-09-391-104-25 Sequence 25, Appl

29 188 61.2 480 4 US-09-949-016-10560 Sequence 10560, A

30 179 58.3 471 4 US-08-994-689C-1 Sequence 1, Appl

31 172 56.0 471 4 US-08-994-689C-21 Sequence 21, Appl

32 164 53.4 513 4 US-09-862-631-4 Sequence 4, Appl

33 160 52.1 264 3 US-09-009-156-6 Sequence 6, Appl

34 160 52.1 264 3 US-09-372-154-6 Sequence 6, Appl

35 160 52.1 267 3 US-08-448-489-18 Sequence 18, Appl

36 160 52.1 267 3 US-09-391-104-27 Sequence 27, Appl

37 160 52.1 267 3 US-09-689-730-18 Sequence 18, Appl

38 160 52.1 271 3 US-08-896-062-2 Sequence 2, Appl

39 160 52.1 277 4 US-09-949-016-8131 Sequence 8131, Ap

40 160 52.1 470 3 US-08-068-392-2 Sequence 2, Appl

41 160 52.1 470 3 US-08-396-988-2 Sequence 2, Appl

42 160 52.1 470 3 US-09-391-104-26 Sequence 26, Appl

43 160 52.1 473 4 US-09-949-016-10876 Sequence 10876, A

44 160 52.1 663 4 US-09-194-468A-30 Sequence 30, Appl

45 159 51.8 135 4 US-09-513-999C-4163 Sequence 4163, Ap

ALIGNMENTS

RESULT 1

US-09-178-002-2

; Sequence 2, Application US/09178002

; Patent No. H001973

; GENERAL INFORMATION:

; APPLICANT: Hu, Shou-Ih

; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant

; FILE REFERENCE: CGC 2048

; CURRENT APPLICATION NUMBER: US/09/178,002

; CURRENT FILING DATE: 1998-10-22

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 2

; LENGTH: 444

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-178-002-2

Query Match 100.0%; Score 307; DB 1; Length 444;

Best Local Similarity 100.0%; Pred. No. 5.6e-32;

Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGPKWERTNLTIRNY 55

Db 43 MQRFFGLNVTGKNEETLDMKKPCRGVPSGGFMLTPGPKWERTNLTIRNY 97

RESULT 2

US-08-704-711A-17

; Sequence 17, Application US/08704711A

; Patent No. 6114159

; GENERAL INFORMATION:

; APPLICANT: WILL, Horst

; APPLICANT: HINZMANN, Bernd

; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX

; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; PRIOR APPLICATION DATA: DE 4438838.1
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-704-711A-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 3
US-09-521-220-17
; Sequence 17, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILZ, Horst
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 466 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-521-220-17

Query Match 100.0%; Score 307; DB 3; Length 466;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 4
US-09-178-002-4
; Sequence 4, Application US/09178002
; Patent No. H001973
; GENERAL INFORMATION:
; APPLICANT: Hu, Shou-Ih
; TITLE OF INVENTION: Human Neutrophil Collagenase Splice Variant
; FILE REFERENCE: CGC 2048
; CURRENT APPLICATION NUMBER: US/09/178,002
; CURRENT FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 4
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-178-002-4

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNBETLDMKKPCRGVDSGGFMLTPGNPKWERTNLTIRNY 120

RESULT 5
US-09-391-104-24
; Sequence 24, Application US/09391104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match 100.0%; Score 307; DB 3; Length 467;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 120

RESULT 6

US-08-448-489-13
; Sequence 13, Application US/08448489
; Patent No. 6184022
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-13

Query Match 100.0%; Score 307; DB 3; Length 468;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 120

RESULT 7

US-09-689-730-13
; Sequence 13, Application US/09689730
; Patent No. 6825024
; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/09/689,730
; CURRENT FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: US/08/448,489
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 13
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: X = UNKNOWN
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-09-689-730-13

Query Match 100.0%; Score 307; DB 4; Length 468;
Best Local Similarity 100.0%; Pred. No. 6e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 120

RESULT 8

US-08-704-711A-16
; Sequence 16, Application US/08704711A
; Patent No. 6114159
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; TITLE OF INVENTION: METALLOPROTEASES, THEIR PRODUCTION AND USE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,711A
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE95/00357
; FILING DATE: 17-MAR-1995
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-704-711A-16

Query Match 72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 67 MQRFFGLNVTGKNEETLDMKKPCGVPDGGFMLTPGNPKWERTNLTIRINY 121

RESULT 9

US-08-448-489-12
; Sequence 12, Application US/08448489
; Patent No. 6184022

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; GENERAL INFORMATION:
; APPLICANT: SEIKI, Motoharu
; APPLICANT: SATO, Hiroshi
; APPLICANT: SHINAGAWA, Akira
; TITLE OF INVENTION: NOVEL METALLOPROTEINASE AND ENCODING DNA THEREFOR
; FILE REFERENCE: 55-290P
; CURRENT APPLICATION NUMBER: US/08/448,489
; CURRENT FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Known Member of
; OTHER INFORMATION: Matrix Metalloproteinase Family
US-08-448-489-12

Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQHTLTIRNY 121

RESULT 10
US-09-521-220-16
; Sequence 16, Application US/09521220
; Patent No. 6399348
; GENERAL INFORMATION:
; APPLICANT: WILL, Horst
; APPLICANT: HINZMANN, Bernd
; TITLE OF INVENTION: DNA SEQUENCES FOR MATRIX
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/521,220
; FILING DATE: 08-Mar-2000
; CLASSIFICATION: <Unknown>
; 21-OCT-1994
; 17-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/704,711
; FILING DATE: <Unknown>
; APPLICATION NUMBER: DE 4438838.1
; FILING DATE: 21-OCT-1994
; APPLICATION NUMBER: DE 4409663.1
; FILING DATE: 17-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 26083/124
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 469 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-521-220-16

Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDPDSCGFMLTGPNKWKERTNLTIRNY 55
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQHTLTIRNY 121

RESULT 11
US-09-391-104-23
; Sequence 23, Application US/093911104
; Patent No. 6399371
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; TITLE OF INVENTION: OF USING SAME
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-23

Query Match          72.0%; Score 221; DB 3; Length 469;
Best Local Similarity 70.9%; Pred. No. 1.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDPDSCGFMLTGPNKWKERTNLTIRNY 55
Db 67 MQEFFGLKVTGKPDATLTKVMKQPRCGVDPDVAQFVLTEGNPRWEQHTLTIRNY 121

RESULT 12
US-09-949-016-6223
; Sequence 6223, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6223
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Human
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GenCore version 5.1.6
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OM protein - protein search, using sw model

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(without alignments)
59.268 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKNEETLDM.....LTFGNPKWERTNLTIRNY 55

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Total number of hits satisfying chosen parameters: 1462099

Minimum DB seq length: 0

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Maximum Match 100%

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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	307	100.0	55	14	US-10-153-185-10
3	307	100.0	55	14	US-10-219-561-10
4	307	100.0	55	16	US-10-032-376A-10
5	307	100.0	55	16	US-10-335-207-10
6	307	100.0	467	9	US-09-391-104-24
7	307	100.0	467	9	US-09-801-196-20
8	307	100.0	467	10	US-09-759-130B-176
9	307	100.0	467	14	US-10-131-985-31
10	307	100.0	467	16	US-10-741-790-176
11	307	100.0	467	17	US-10-741-600-917
12	307	100.0	467	17	US-10-901-417-31
13	221	72.0	454	15	US-10-115-479-32

14	221	72.0	454	15	US-10-115-479-34	Sequence 34, Appl
15	221	72.0	454	15	US-10-115-479-36	Sequence 36, Appl
16	221	72.0	454	15	US-10-115-479-38	Sequence 38, Appl
17	221	72.0	469	9	US-09-391-104-23	Sequence 23, Appl
18	221	72.0	469	9	US-09-801-196-19	Sequence 19, Appl
19	221	72.0	469	9	US-09-853-386-100	Sequence 100, Appl
20	221	72.0	469	14	US-10-301-822-119	Sequence 119, Appl
21	221	72.0	469	14	US-10-021-660-76	Sequence 76, Appl
22	221	72.0	469	14	US-10-308-279-34	Sequence 34, Appl
23	221	72.0	469	14	US-10-131-985-23	Sequence 23, Appl
24	221	72.0	469	15	US-10-295-027-12	Sequence 12, Appl
25	221	72.0	469	15	US-10-295-027-14	Sequence 14, Appl
26	221	72.0	469	15	US-10-295-027-1167	Sequence 1167, Appl
27	221	72.0	469	15	US-10-295-027-1168	Sequence 1168, Appl
28	221	72.0	469	15	US-10-115-479-30	Sequence 30, Appl
29	221	72.0	469	15	US-10-115-479-40	Sequence 40, Appl
30	221	72.0	469	15	US-10-211-462-22	Sequence 22, Appl
31	221	72.0	469	15	US-10-188-832-6	Sequence 6, Appl
32	221	72.0	469	16	US-10-734-564-109	Sequence 109, Appl
33	221	72.0	469	17	US-10-901-417-23	Sequence 23, Appl
34	221	72.0	470	15	US-10-447-315-1	Sequence 1, Appl
35	221	72.0	496	14	US-10-106-698-6283	Sequence 6283, Appl
36	214	69.7	54	14	US-10-219-329-9	Sequence 9, Appl
37	214	69.7	54	14	US-10-153-185-9	Sequence 9, Appl
38	214	69.7	54	14	US-10-219-561-9	Sequence 9, Appl
39	214	69.7	54	16	US-10-032-376A-9	Sequence 9, Appl
40	214	69.7	54	16	US-10-335-207-9	Sequence 9, Appl
41	198	64.5	173	15	US-10-115-479-48	Sequence 48, Appl
42	196	63.8	267	14	US-10-133-797-73	Sequence 73, Appl
43	196	63.8	477	9	US-09-391-104-21	Sequence 21, Appl
44	196	63.8	477	9	US-09-801-196-24	Sequence 24, Appl
45	196	63.8	477	14	US-10-171-311-137	Sequence 137, Appl

ALIGNMENTS

RESULT 1

US-10-219-329-10
; Sequence 10, Application US/10219329
; Publication No. US20030096757A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Anti-Cancer and Wound Healing Compounds
; FILE REFERENCE: 1443 035WO1
; CURRENT APPLICATION NUMBER: US/10/219,329
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-329-10

Query Match 100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMTPGNPKWERTNLTIRNY 55

Db 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMTPGNPKWERTNLTIRNY 55

RESULT 2

US-10-153-185-10
; Sequence 10, Application US/10153185
; Publication No. US20030148959A1

```
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.034US1
; CURRENT APPLICATION NUMBER: US/10/153,185
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-153-185-10

Query Match          100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 3
US-10-219-561-10
; Sequence 10, Application US/10219561
; Publication No. US20030166567A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Stephen
; APPLICANT: Malik, Sohail
; APPLICANT: Villanueva, Julie M.
; TITLE OF INVENTION: Anti-Aging and Wound Healing Compounds
; FILE REFERENCE: 1443.008US2
; CURRENT APPLICATION NUMBER: US/10/219,561
; CURRENT FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: US 10/032,376
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 10/153,185
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-219-561-10

Query Match          100.0%; Score 307; DB 14; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 4
US-10-032-376A-10
; Sequence 10, Application US/10032376A
; Publication No. US20040127420A1
; GENERAL INFORMATION:
; APPLICANT: Quirk, Steven
; TITLE OF INVENTION: Metalloproteinase Inhibitors for Wound Healing
; FILE REFERENCE: 1443.008US1
; CURRENT APPLICATION NUMBER: US/10/032,376A
; CURRENT FILING DATE: 2001-12-21
```

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; PRIOR APPLICATION NUMBER: 60/312,726
; PRIOR FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-032-376A-10

Query Match          100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 5
US-10-335-207-10
; Sequence 10, Application US/10335207
; Publication No. US20040127421A1
; GENERAL INFORMATION:
; APPLICANT: Malik, Sohail
; APPLICANT: Quirk, Stephen
; TITLE OF INVENTION: Method to Increase Fibronectin
; FILE REFERENCE: 1443.047US1
; CURRENT APPLICATION NUMBER: US/10/335,207
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-335-207-10

Query Match          100.0%; Score 307; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 7.5e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55
Db 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRNY 55

RESULT 6
US-09-391-104-24
; Sequence 24, Application US/09391104
; Publication No. US20020031817A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Falduto, Michael T.
; APPLICANT: Magnuson, Scott R.
; APPLICANT: Morgan, Douglas W.
; TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
; TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
; FILE REFERENCE: 6073.US.P1
; CURRENT APPLICATION NUMBER: US/09/391,104
; CURRENT FILING DATE: 1999-09-07
; PRIOR APPLICATION NUMBER: US 08/814,394
; PRIOR FILING DATE: 1997-03-11
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-391-104-24

Query Match          100.0%; Score 307; DB 9; Length 467;
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; Best Local Similarity 100.0%; Pred. No. 9.4e-32;
; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 7
US-09-801-196-20
; Sequence 20, Application US/09801196
; Patent No. US20020037827A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Kai
; APPLICANT: Smith, Ryan
; APPLICANT: Fajardo, Mark
; APPLICANT: Moss, Patrick
; TITLE OF INVENTION: A NOVEL MATRIX METALLOPROTEINASE (MMP-25)
; FILE REFERENCE: 240083.509
; CURRENT FILING DATE: 2001-03-06
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-801-196-20

Query Match 100.0%; Score 307; DB 9; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 8
US-09-759-130B-176
; Sequence 176, Application US/09759130B
; Publication No. US2003002279A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J
; APPLICANT: Mackay, Charles R
; APPLICANT: Myers, Paul S
; APPLICANT: Leiby, Kevin R
; APPLICANT: Wrighton, Nicolas
; APPLICANT: Goodearl, Andrew
; APPLICANT: Holtzman, Douglas A
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
; TITLE OF INVENTION: USBS.
; FILE REFERENCE: MPI00-5350NMIM
; CURRENT APPLICATION NUMBER: US/09759,130B
; CURRENT FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2002-09-16
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 2000-04-27
; PRIOR FILING DATE: 2000-05-24
; PRIOR FILING DATE: 1999-06-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/559,497
; PRIOR APPLICATION NUMBER: US 09/578,063
; PRIOR APPLICATION NUMBER: US 09/333,159
; PRIOR APPLICATION NUMBER: US 09/596,194
; PRIOR APPLICATION NUMBER: US 09/342,364

```

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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: US 09/608,452
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/393,996
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 09/602,871
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 09/420,707
; PRIOR FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-130B-176

Query Match 100.0%; Score 307; DB 10; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 9
US-10-131-985-31
; Sequence 31, Application US/10131985
; Publication No. US20030199440A1
; GENERAL INFORMATION:
; APPLICANT: Dack, Kevin N
; APPLICANT: Davies, Michael J
; APPLICANT: Fish, Paul V
; APPLICANT: Huggins, Jonathan P
; APPLICANT: McIntosh, Fraser S
; APPLICANT: Ocleston, Nicholas L
; TITLE OF INVENTION: Composition
; FILE REFERENCE: PCS 10391A
; CURRENT APPLICATION NUMBER: US/10/131,985
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US/09/726,295
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: GB 9930768.8
; PRIOR FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-985-31

Query Match 100.0%; Score 307; DB 14; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDSGGFMLTGGNPKWERTNLTIRNY 120

RESULT 10
US-10-741-790-176
; Sequence 176, Application US/10741790
; Publication No. US20040121396A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: McCarthy, Sean A
; APPLICANT: Fraser, Christopher C
; APPLICANT: Sharp, John D
; APPLICANT: Barnes, Thomas S
; APPLICANT: Kirst, Susan J

```



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/ APPLICANT: Mackay, Charles R
/ APPLICANT: Myers, Paul S
/ APPLICANT: Leiby, Kevin R
/ APPLICANT: Wrighton, Nicolas
/ APPLICANT: Goodearl, Andrew
/ APPLICANT: Holtzman, Douglas A
/ TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
/ TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
/ TITLE OF INVENTION: USGS.
/ FILE REFERENCE: MP100-535OMNIM
/ CURRENT APPLICATION NUMBER: US/10/741,790
/ PRIOR FILING DATE: 2003-12-19
/ PRIOR APPLICATION NUMBER: US 09/479,249
/ PRIOR FILING DATE: 2000-01-07
/ PRIOR APPLICATION NUMBER: US 09/559,497
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/578,063
/ PRIOR FILING DATE: 2000-05-24
/ PRIOR APPLICATION NUMBER: US 09/333,159
/ PRIOR FILING DATE: 1999-06-14
/ PRIOR APPLICATION NUMBER: US 09/596,194
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: US 09/342,364
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: US 09/608,452
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/393,996
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US 09/602,871
/ PRIOR FILING DATE: 2000-06-23
/ PRIOR APPLICATION NUMBER: US 09/420,707
/ PRIOR FILING DATE: 1999-10-19
/ NUMBER OF SEQ ID NOS: 460
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 176
/ LENGTH: 467
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-741-790-176

Query Match 100.0%; Score 307; DB 16; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 11
US-10-741-600-917
/ Sequence 917, Application US/10741600
/ Publication No. US20050026169A1
/ GENERAL INFORMATION:
/ APPLICANT: CARGILL, Michele et al.
/ TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
/ TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001499
/ CURRENT APPLICATION NUMBER: US/10/741,600
/ CURRENT FILING DATE: 2003-12-22
/ NUMBER OF SEQ ID NOS: 7397
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 917
/ LENGTH: 467
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-741-600-917

Query Match 100.0%; Score 307; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 12
US-10-901-417-31
/ Sequence 31, Application US/10901417
/ Publication No. US20050026936A1
/ GENERAL INFORMATION:
/ APPLICANT: Dack, Kevin N
/ APPLICANT: Davies, Michael J
/ APPLICANT: Fish, Paul V
/ APPLICANT: Huggins, Jonathan P
/ APPLICANT: McIntosh, Fraser S
/ APPLICANT: Occleston, Nicholas L
/ TITLE OF INVENTION: Composition
/ FILE REFERENCE: PCS 10391A
/ CURRENT APPLICATION NUMBER: US/10/901,417
/ CURRENT FILING DATE: 2004-07-28
/ PRIOR APPLICATION NUMBER: US/10/131,985
/ PRIOR FILING DATE: 2002-04-25
/ PRIOR APPLICATION NUMBER: US/09/726,295
/ PRIOR FILING DATE: 2000-11-30
/ PRIOR APPLICATION NUMBER: GB 9930768.8
/ PRIOR FILING DATE: 1999-12-29
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 31
/ LENGTH: 467
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-901-417-31

Query Match 100.0%; Score 307; DB 17; Length 467;
Best Local Similarity 100.0%; Pred. No. 9.4e-32;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 66 MORFFGLNVTGKPNBETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 120

RESULT 13
US-10-115-479-32
/ Sequence 32, Application US/10115479
/ Publication No. US20040006205A1
/ GENERAL INFORMATION:
/ APPLICANT: Li, Li
/ APPLICANT: Gerlach, Valerie L.
/ APPLICANT: Liu, Xiaohong
/ APPLICANT: Miller, Charles E.
/ APPLICANT: Spytek, Kimberly A.
/ APPLICANT: Zerhusen, Bryan D.
/ APPLICANT: Pena, Carol E.A.
/ APPLICANT: Shenoy, Suresh G.
/ APPLICANT: Zhong, Haihong
/ APPLICANT: Smithson, Glenda
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Boldog, Ferenc L.;
/ APPLICANT: Voss, Edward
/ APPLICANT: Vernet, Corine
/ APPLICANT: MacDougall, John A.
/ APPLICANT: Rastelli, Luca
/ APPLICANT: Anderson, David W.
/ APPLICANT: Zhong, Mei
/ APPLICANT: Mezes, Peter S.
/ APPLICANT: Furtak, Katarzyna
/ APPLICANT: Patturajan, Meera
/ APPLICANT: Burgess, Catherine E.
/ APPLICANT: Malyancker, Uriel M.
/ APPLICANT: Shinkets, Richard A.
/ APPLICANT: Taupier, Raymond J.
/ APPLICANT: Edinger, Shlomit R.
```

```

; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 32
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-32

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Query Match      72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

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QY 1 MQRFFGLNVTGKNEETLDMMKPRCGVPSDGGFMLTPGNPKWERTNLTIRNY 55
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Db 50 MQEFGGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLTIRNY 104

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RESULT 14
US-10-115-479-34
; Sequence 34, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.

```

```

; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 34
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-34

```

```

Query Match      72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```

```

QY 1 MQRFFGLNVTGKNEETLDMMKPRCGVPSDGGFMLTPGNPKWERTNLTIRNY 55
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 50 MQEFGGLKVTGKPDATLTKVMKQPRCGVDPVAQFVLTEGNPRWEQTHLTIRNY 104

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RESULT 15
US-10-115-479-36
; Sequence 36, Application US/10115479
; Publication No. US20040006205A1
; GENERAL INFORMATION:
; APPLICANT: Li, Li
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Miller, Charles E.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Zhong, Haihong
; APPLICANT: Smithson, Glendda
; APPLICANT: Casman, Stacie J.
; APPLICANT: Boldog, Ferenc L.;
; APPLICANT: Voss, Edward
; APPLICANT: Vernet, Corine
; APPLICANT: MacDougall, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Anderson, David W.
; APPLICANT: Zhong, Mei
; APPLICANT: Mezes, Peter S.
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Malyanker, Uriel M.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Edinger, Shlomit R.

```

```

; APPLICANT: Mazur, Ann
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-322 B (Cura 622 PT)
; CURRENT APPLICATION NUMBER: US/10/115,479
; CURRENT FILING DATE: 2002-11-18
; PRIOR APPLICATION NUMBER: 60/281,136
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/281,863
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/281,906
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/282,934
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: 60/283,657
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,678
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,687
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/283,710
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: 60/284,234
; PRIOR FILING DATE: 2001-04-17
; PRIOR APPLICATION NUMBER: 60/285,325
; PRIOR FILING DATE: 2001-04-19
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 198
; SEQ ID NO 36
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-115-479-36

```

```

Query Match      72.0%; Score 221; DB 15; Length 454;
Best Local Similarity 70.9%; Pred. No. 2.1e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

```

```

Qy      1  MQRFFGLNVTGKPNETLDMKKPRCGVDPDSGGFMLTPGNPKWERTNLTIRINY 55
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      50  MQEFFFGLKVTGRDAETLKMVKQPRCGVDPVAQFVLTEGNPRWEQTHLTIRINY 104

```

Search completed: May 27, 2005, 07:34:00
Job time : 321.128 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 106.827 Seconds
(without alignments)
199.124 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGRPNSTLDM.....LTPGNPKWERTNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 segs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001s:*

5: Geneseq2002s:*

6: Geneseq2003as:*

7: Geneseq2003bs:*

8: Geneseq2004s:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	55	6	ABP97132 Human mat
2	307	100.0	55	6	ABG76318 Human mat
3	307	100.0	55	8	ADQ17093 Human mat
4	307	100.0	444	4	AAG65357 Human MMP
5	307	100.0	467	4	AAB84610 Amino aci
6	307	100.0	467	4	Aae10416 Human mat
7	307	100.0	467	4	AAG65358 Human neu
8	307	100.0	467	6	ABo32581 Secreted
9	307	100.0	467	8	ADQ10212 Human pol
10	307	100.0	467	8	ADQ39254 Human myo
11	226	73.6	454	8	ADL93947 Human G-c
12	221	72.0	454	7	ADL16002 G-coupled
13	221	72.0	454	7	ADL16004 G-coupled
14	221	72.0	454	7	ADL16008 G-coupled
15	221	72.0	454	7	ADL16006 G-coupled
16	221	72.0	454	8	ADL93945 Human G-c
17	221	72.0	454	8	ADL93943 Human G-c
18	221	72.0	455	8	ADL93941 Human G-c
19	221	72.0	469	4	AAB84606 Amino aci
20	221	72.0	469	4	Aae10415 Human mat
21	221	72.0	469	6	ABU03466 Angiogene
22	221	72.0	469	6	ABR58543 Human can
23	221	72.0	469	6	ABR58542 Human can
24	221	72.0	469	6	ABR48148 Human bla
25	221	72.0	469	6	ABU56596 Lung canc

ALIGNMENTS

RESULT 1

ABP97132

ID ABP97132 standard; peptide; 55 AA.

XX AC ABP97132;

DT 24-JUN-2003 (first entry)

DE Human matrix metalloproteinase 8 cleavage region peptide SEQ ID NO:10.

XX Human, matrix metalloproteinase; MMP; anticancer; wound healing;
KW matrix metalloproteinase inhibitor; antitumor; antiangiogenic; cardiant;
KW vascular endothelial growth factor inhibitor; VEGF inhibitor; cytostatic;
KW vulnary; cerebroprotective; antidiabetic; ophthalmological; tumour;
KW dermatological; metastatic; non-metastatic; vascularised; heart disease;
KW non-vascularised; surgical incision; chronic wound; stroke; angiogenesis;
KW macular degeneration; diabetic retinopathy; cleavage region.

OS Homo sapiens.

XX XX

PN WO2003018748-A2.

XX XX

PD 06-MAR-2003.

XX 15-AUG-2002; 2002WO-US026319.

XX 16-AUG-2001; 2001US-0312726P.

PR 21-DEC-2001; 2001US-00032376.

PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.

PI Quirk S, Weart IP;

XX WPI; 2003-391408/36.

DR Anti-angiogenic composition comprising peptide inhibitor of matrix

XX metalloproteinase, useful for decreasing the expression of vascular

PT endothelial growth factor and treating cancers and tissue injuries.

XX Claim 17; Page 16; 103pp; English.

PS The present invention describes an anti-angiogenic composition (I) for

XX inhibiting expression of vascular endothelial growth factor (VEGF). (I)

CC comprises an effective amount of a peptide inhibitor of matrix

CC metalloproteinase (MMP), where the peptide can inhibit the expression of

CC VEGF. (I) has cytostatic, vulnerary, cardiant, cerebroprotective,

CC antidiabetic, ophthalmological and dermatological activities. (I) can be

Abu56597 Lung canc
Abu07454 Protein d
Abp54454 Matrix me
Adb79176 Matrix me
Adn34550 Human aki
Ade16000 G-coupled
Ade16010 G-coupled
Adn39849 Cancer/an
Adn38694 Cancer/an
Adn38696 Cancer/an
Adn39850 Cancer/an
Adn95538 Human BEC
Adl99949 Human G-c
Adl99339 Human G-c
Adq29683 Human col
Adsl9177 Human mat
Adn07695 Human mat
Ade07892 Novel pro
Aag75509 Human col
Aap93628 Sequence

CC used for inhibiting expression of VEGF, and so can be used for inhibiting
 CC growth of tumours and diminishing tumours size. The tumour can be
 CC metastatic, non-metastatic, vascularised, non-vascularised, hard or soft.
 CC (I) is also useful for treating injuries including wounds, surgical
 CC incisions, chronic wounds, heart diseases and stroke. (I) is also useful
 CC for treating disorders characterised by excessive angiogenesis e.g.
 CC macular degeneration and diabetic retinopathy. The present sequence
 CC represents a human MMP cleavage region peptide, which is used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 55 AA;

Query Match 100.0%; Score 307; DB 6; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55

RESULT 2
 ABG76318
 ID ABG76318 standard; protein; 55 AA.
 XX
 AC ABG76318;
 XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human matrix metalloproteinase (MMP) peptide inhibitor #10.
 XX
 KW Human; peptide inhibitor; matrix metalloproteinase-8; MMP-8;
 KW cleavage region; proenzyme form; cellular proliferation; fibroblast;
 KW keratinocyte; healthy skin development; wound healing; scarring;
 KW skin tone; wrinkle; anti-aging; vulnerary.
 XX
 OS Homo sapiens.

XX
 PN WO2003016520-A1.
 XX
 PD 27-FEB-2003.

XX 15-AUG-2002; 2002WO-US026198.
 XX 16-AUG-2001; 2001US-0312726P.
 PR 21-DEC-2001; 2001US-00032376.
 PR 21-MAY-2002; 2002US-00153185.

XX (KIMB) KIMBERLY-CLARK WORLDWIDE INC.
 PA
 PI Quirk S, Malik S, Villanueva JM;
 XX
 DR WPI; 2003-289980/28.

XX Novel peptide inhibitor of proteinase activity of matrix
 PT metalloproteinases, e.g. matrix metalloproteinase-2, useful for
 PT stimulating cellular proliferation of fibroblasts or keratinocytes.

XX Claim 1; Page 16; 120pp; English.

XX The present invention relates to peptide inhibitors of metalloproteinases
 CC (MMPs), particularly metalloproteinase-2 (MMP-2). The inhibitors have
 CC peptide sequences related to the cleavage regions of the proenzyme forms
 CC of the MMPs. The peptide inhibitors are useful for stimulating cellular
 CC proliferation of fibroblasts or keratinocytes, promoting healthy skin
 CC development, treating and preventing scarring, improving skin tone,
 CC reducing wrinkling and for simulating the development of smooth, healthy
 CC skin. The peptide inhibitors are useful as anti-aging and wound healing
 CC compounds. ABG76309-ABG76321 represent peptide inhibitors of MMPs

XX Sequence 55 AA;
 SQ
 Query Match 100.0%; Score 307; DB 6; Length 55;

Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55

RESULT 3
 ADQ17093
 ID ADQ17093 standard; peptide; 55 AA.
 XX
 AC ADQ17093;
 XX
 DT 23-SEP-2004 (first entry)
 XX

DE Human matrix metalloproteinase-8 (MMP8) cleavage region peptide.
 XX
 KW Fibronectin; healthy skin; wrinkle; wound; vulnerary; dermatological;
 KW human; matrix metalloproteinase; MMP.
 XX
 OS Homo sapiens.

XX
 PN US2004127421-A1.
 XX
 PD 01-JUL-2004.
 XX

PF 30-DEC-2002; 2002US-00335207.
 XX
 PR 30-DEC-2002; 2002US-00335207.

XX (WALI/) MALIK S.
 PA (QUIR/) QUIRK S.
 XX
 PI Malik S, Quirk S;
 XX
 DR WPI; 2004-506456/48.

XX Composition used for preventing and treating wrinkles and treating wounds
 PT comprises peptide having sequence related to matrix metalloproteinase
 PT proenzyme.
 XX
 PS Example 1; SEQ ID NO 10; 60pp; English.

XX The present invention provides peptides and compositions containing such
 CC peptides that are useful as agents to maintain healthy skin and to
 CC promote the condition of the skin. The invention is useful for increasing
 CC the amount of fibronectin in tissue. The invention is also useful for
 CC encouraging the maintenance and development of healthy skin, preventing
 CC and treating wrinkles and for treating wounds. The invention acts as
 CC vulnerary and dermatological agents. The present sequence is human matrix
 CC metalloproteinase (MMP) cleavage region peptide. This sequence is used in
 CC the exemplification of the invention.

XX Sequence 55 AA;
 SQ
 Query Match 100.0%; Score 307; DB 8; Length 55;
 Best Local Similarity 100.0%; Pred. No. 3.6e-34;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55
 Db 1 MQRFFGLNVTGKPNBETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTIRINY 55

RESULT 4
 AAG65357
 ID AAG65357 standard; protein; 444 AA.
 XX
 AC AAG65357;
 XX
 DT 30-NOV-2001 (first entry)
 XX

```
DB Human MMP-8alt polypeptide.
XX MMP-8alt; MMP-8; matrix metalloproteinase; neutrophil collagenase;
XX anti-arthritis; cytoskeletal; anti-Parkinsonian; neuroprotective;
KW nontropic; cancer; apoptosis; Parkinson's disease; Alzheimer's disease;
KW Huntington's disease; human; splice variant.
XX Homo sapiens.
XX US1973-H.
XX 03-JUL-2001.
XX 22-OCT-1998; 98US-00178002.
XX 22-OCT-1998; 98US-00178002.
XX (NOVS ) NOVARTIS AG.
XX Hu S;
XX WPI: 2001-431511/46.
XX N-PSDB; AAH47515.
XX New MMP-8alt polynucleotides and polypeptides useful as research reagents
XX and materials for discovering treatments and diagnostics to human
XX disease, or as targets for identifying inhibitors of MMP-8alt expression.
XX Claim 11; Col 25-30; 25pp; English.
XX The invention relates to human MMP-8alt polypeptide and polynucleotides.
XX MMP-8alt is a splice variant of the MMP-8 (matrix metalloproteinase)
XX cDNA. The MMP-8alt polypeptide can be expressed by standard recombinant
XX methodology. The polynucleotides and polypeptides may be used as research
XX reagents and materials for the discovery of treatments and diagnostics to
XX human disease, and as targets for identifying modulators. Inhibitors of
XX MMP-8alt polynucleotide or polypeptide expression may be used to treat
XX and/or prevent arthritis, cancer and cancer metastasis, and diseases
XX caused by cellular apoptosis including Parkinson's disease, Alzheimer's
XX disease and Huntington's disease. The present sequence represents the
XX human MMP-8alt polypeptide
XX
SQ Sequence 444 AA;
Query Match 100.0%; Score 307; DB 4; Length 444;
Best Local Similarity 100.0%; Pred. No. 4.7e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGPNKWTNLTIRNY 55
Db 43 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGPNKWTNLTIRNY 97
RESULT 5
AAB84610
ID AAB84610 standard; protein; 467 AA.
XX
XX AAB84610;
AC
XX
XX 05-SEP-2001 (first entry)
DT
XX
XX Amino acid sequence of matrix metalloproteinase-8.
DE
XX
XX Growth factor; protein inhibitor; protease; damaged tissue;
KW platelet-derived growth factor; PDGF; fibroblast growth factor; FGF;
KW connective tissue derived growth factor; CTGF; chrysalin; VEGF;
KW keratinocyte-derived growth factor; KGF; epidermal growth factor; EGF;
KW transforming growth factor-beta; TGF-beta; matrix metalloproteinase; MMP;
KW granulocyte macrophage colony stimulating factor; GM-CSF; uPA;
KW vascular endothelial growth factor; urokinase plasminogen activator;
KW dermal ulcer; wound.
XX
XX Homo sapiens.
OS
```

```
XX WO200149309-A2.
XX
XX 12-JUL-2001.
XX
XX 21-DEC-2000; 2000WO-1B001935.
XX
XX 29-DEC-1999; 99GB-00030768.
XX
XX (PFIZ ) PFIZER LTD.
XX (PFIZ ) PFIZER INC.
XX
XX Davies MJ, Huggins JP, McIntosh FS, Occleston NL;
XX WPI: 2001-418351/44.
XX N-PSDB; AAH28225.
XX
XX Composition for the treatment of damaged tissue i.e. chronic wounds and
XX dermal ulcers comprises an inhibitor agent i.e. a protease and a growth
XX factor.
XX
XX Disclosure; Page 555; 572pp; English.
XX
XX The specification describes a pharmaceutical composition, comprising a
XX growth factor, an inhibitor agent, i.e. a protease. The inhibitor agent
XX inhibits the action of at least one specific adverse protein, i.e. a
XX protease, that is upregulated in a damaged tissue such as a wound
XX environment. Growth factors which are included in the composition of the
XX invention are platelet-derived growth factor (PDGF), fibroblast growth
XX factor (FGF), connective tissue derived growth factor (CTGF),
XX keratinocyte-derived growth factor (KGF), transforming growth factor-beta
XX (TGF-beta), granulocyte macrophage colony stimulating factor (GM-CSF),
XX epidermal growth factor (EGF), vascular endothelial growth factor (VEGF),
XX and chrysalin. Inhibitors which are included in the composition of the
XX invention include inhibitors of urokinase-type plasminogen activator
XX (uPA) and matrix metalloproteinase (MMP). The composition is useful for
XX the treatment of chronic damaged tissue, i.e. wounds and dermal ulcers.
XX The present sequence represents a human MMP-8, and is used to produce the
XX composition of the invention
XX
XX Sequence 467 AA;
Query Match 100.0%; Score 307; DB 4; Length 467;
Best Local Similarity 100.0%; Pred. No. 4.9e-33;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGPNKWTNLTIRNY 55
Db 66 MQRFFGLNVTGKNEETLDMKKPCRCVPSGSGFMLTPGPNKWTNLTIRNY 120
RESULT 6
AAE10416
ID AAE10416 standard; protein; 467 AA.
XX
XX AAE10416;
AC
XX
XX 10-DEC-2001 (first entry)
DT
XX
XX Human matrix metalloproteinase-8 (MMP-8) protein.
DE
XX
XX Human; matrix metalloproteinase; MMP-8; hair growth; antisense therapy;
KW endopeptidase; skin cell; breast cancer; hair follicle; chromosome 11q22.
XX
XX Homo sapiens.
OS
XX Key Location/Qualifiers
XX Peptide 1..20 /label= Signal_peptide
XX Protein 21..467 /label= Mature_MMP_8_protein
XX Domain 89..95 /label= Cysteine_switch_domain
XX
```



```

PA (FRASER) FRASER C C.
PA (BARN) BARNES T M.
PA (SHAR) SHARP J D.
PA (KIRS) KIRST S J.
PA (MYER) MYERS P S.
PA (LEIB) LEIBY K R.
PA (HOLT) HOLTZMAN D A.
PA (MCCA) MCCARTHY S A.
PA (WRIG) WRIGHTON N.
PA (MACK) MACKAY C R.
PA (GOOD) GOODEARL A D J.
XX
XX
PI FRASER CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
PI Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX
XX WPI; 2003-456290/43.
XX N-PSDB; ACD66741.
XX
XX New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202,
XX TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or
XX treating disorders such as cancer, diabetes or atherosclerosis, and in
XX forensic biology.
XX
XX Disclosure; Fig 15V-15W; 482pp; English.
XX
XX The invention relates to secreted polypeptide-related proteins and
XX nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The
XX nucleic acids, proteins and antibodies specific to the proteins are
XX useful in screening assays, predictive medicine (e.g. diagnostic assays,
XX prognostic assays, monitoring clinical trials and pharmacogenetics) and
XX prophylactic and therapeutic methods. The sequences are used in
XX diagnosing, preventing or treating proliferative disorders (e.g.
XX cancers), hormonal disorders (e.g. diabetes or thyroid disorders), immune
XX disorders (e.g. multiple sclerosis or lupus), neurological disorders
XX (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular
XX disorders (e.g. myocardial infarction or congestive heart disease), blood
XX platelet disorders (e.g. thrombocytopenia or anaemia) and disorders
XX involving blood vessels (e.g. atherosclerosis or vasculitis). The nucleic
XX acids may also be used in chromosome mapping, tissue typing and forensic
XX biology, and as surrogate markers. This sequence represents a secreted
XX polypeptide-related protein of the invention. Note: The sequence data for
XX this patent was obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html
XX
XX Sequence 467 AA;
XX
XX Query Match 100.0%; Score 307; DB 6; Length 467;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-33;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRYNY 55
XX DB 66 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRYNY 120
XX
XX RESULT 9
XX ADQ10212
XX ID ADQ10212 standard; protein; 467 AA.
XX
XX AC ADQ10212;
XX
XX AC ADQ10212;
XX
XX DT 09-SEP-2004 (first entry)
XX
XX DE Human polypeptide #75.
XX
XX Human; cancer; obesity; gastritis; diarrhoea; haemorrhoid; asthma;
XX anaemia; graft-versus-host reaction; allergic reaction; cystic fibrosis;
XX hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;
XX arteriosclerosis; hypertension; bacterial infection; psoriasis;
XX diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
XX Parkinson's disease; AIDS; tuberculosis; viral infection; malaria;
XX goiter; infertility; endometriosis; muscular disorder.
XX

```

```

OS Homo sapiens.
XX
XX US2004121396-A1.
XX
XX 24-JUN-2004.
XX
XX 19-DEC-2003; 2003US-00741790.
XX
XX 14-JUN-1999; 99US-00333159.
XX 29-JUN-1999; 99US-00342364.
XX 10-SEP-1999; 99US-00393996.
XX 19-OCT-1999; 99US-00420707.
XX 07-JAN-2000; 2000US-00479249.
XX 27-APR-2000; 2000US-00559497.
XX 24-MAY-2000; 2000US-00578063.
XX 16-JUN-2000; 2000US-00596194.
XX 23-JUN-2000; 2000US-00602871.
XX 30-JUN-2000; 2000US-00608452.
XX 12-JAN-2001; 2001US-00759130.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Fraser CC, Barnes TM, Sharp JD, Kirst SJ, Myers PS, Leiby KR;
XX Holtzman DA, McCarthy SA, Wrighton N, Mackay CR, Goodearl ADJ;
XX
XX WPI; 2004-479675/45.
XX
XX New TANGO, INTERCEPT, and MANGO, useful in diagnosing, preventing, and
XX treating cancer, constipation, hemorrhoids, cystic fibrosis,
XX hypogonadism, psoriasis, hepatitis, Alzheimer's disease, AIDS,
XX tuberculosis, malaria, goiter, infertility.
XX
XX Disclosure; SEQ ID NO 176; 483pp; English.
XX
XX The invention relates to human polynucleotides and the polypeptides they
XX encode. The invention also relates to a host cell containing a
XX polynucleotide of the invention, an antibody which selectively binds with
XX a polypeptide of the invention, a method of detecting the presence of a
XX polypeptide in a sample, a method of identifying a compound which binds
XX with a polypeptide, and a method of modulating the activity of a
XX polypeptide. The polynucleotides, polypeptides and compositions are
XX useful for diagnosing, preventing and/or treating cancer, obesity,
XX gastritis, diarrhoea, haemorrhoids, asthma, anaemia, graft-versus-host
XX reactions, allergic reactions, cystic fibrosis, hypogonadism,
XX cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
XX hypertension, bacterial infections, psoriasis, diabetes mellitus,
XX hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
XX disease, AIDS, tuberculosis, viral infections, malaria, goiter,
XX infertility, endometriosis, wounds and muscular disorders. This sequence
XX represents a human polypeptide of the invention. Note: The sequence data
XX for this patent did not form part of the printed specification but was
XX obtained in electronic format from USPTO at
XX seqdata.uspto.gov/sequence.html.
XX
XX Sequence 467 AA;
XX
XX Query Match 100.0%; Score 307; DB 8; Length 467;
XX Best Local Similarity 100.0%; Pred. No. 4.9e-33;
XX Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRYNY 55
XX DB 66 MQRFFGLNVTGKNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRYNY 120
XX
XX RESULT 10
XX ADQ39254
XX ID ADQ39254 standard; protein; 467 AA.
XX
XX AC ADQ39254;
XX
XX AC ADQ39254;
XX
XX DT 18-NOV-2004 (first entry)
XX
XX

```

DE Human myocardial infarction-associated gene derived protein, SEQ ID 917.
 XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;
 KW cardiant; gene therapy; human.
 XX Homo sapiens.
 XX OS
 XX WO2004058052-A2.
 XX PN
 XX 15-JUL-2004.
 XX PD
 XX 22-DEC-2003; 2003WO-US040978.
 XX PF
 XX 20-DEC-2002; 2002US-0434778P.
 XX PR
 XX 10-MAR-2003; 2003US-0453135P.
 XX PR
 XX 30-APR-2003; 2003US-0466412P.
 XX PR
 XX 23-SEP-2003; 2003US-0504955P.
 XX PR
 XX (APPL-) APPLERA CORP.
 XX PA
 XX Cargill M, Devlin JJ, Iakoubova O;
 XX PI
 XX WPI; 2004-533949/51.
 XX DR
 XX N-PSDB; ADQ38426.
 XX DR
 XX
 XX PT Identifying an individual who has an altered risk for developing
 PT myocardial infarction by detecting a single nucleotide polymorphism in
 PT the individual's nucleic acids.
 XX PS
 XX Claim 10; SEQ ID NO 917; 145pp; English.
 XX CC
 CC The invention relates to a novel method for identifying an individual who
 CC has an altered risk for developing myocardial infarction. The method
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of
 CC the nucleotide sequences given in the specification in the individual's
 CC nucleic acids, where the presence of the SNP is correlated with an
 CC altered risk for myocardial infarction in the individual. The invention
 CC further comprises: an isolated nucleic acid molecule comprising at least
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in
 CC the specification or its complement and encoding any one of the amino
 CC acid sequences given in the specification; an isolated polypeptide
 CC comprising an amino acid sequence given in the specification; an antibody
 CC that specifically binds to the polypeptide or its antigen-binding
 CC fragment; an amplified polynucleotide containing an SNP given in the
 CC specification and which is between about 16 and 1000 nucleotides in
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a
 CC method for identifying an agent useful in treating or preventing
 CC myocardial infarction. The novel detection method has cardiant activity.
 CC The nucleic acids of the invention may be used in gene therapy. The
 CC method is useful in identifying an individual who has an increased or
 CC decreased risk for developing myocardial infarction and for preparing a
 CC composition for treating or preventing myocardial infarction. This
 CC sequence represents the protein of a human myocardial infarction-
 CC associated gene containing one or more SNP's of the invention. Note: This
 CC sequence was not shown in the specification. The sequence has come from
 CC an electronic sequence listing downloaded from the WIPO website.
 XX CC
 XX SQ Sequence 467 AA;
 Query Match 100.0%; Score 307; DB 8; Length 467;
 Best Local Similarity 100.0%; Pred. NO. 4,9e-33;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQRFFGLVNTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTVIRNY 55
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 66 MQRFFGLVNTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTVIRNY 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 11
 ADL93947
 ID ADL93947 standard; protein; 454 AA.

XX ADL93947;
 XX AC
 XX DT 20-MAY-2004 (first entry)
 XX DE
 XX DE Human G-coupled protein receptor-related protein #19.
 XX KW
 KW human; transgenic; Gene Therapy; Protein Therapy; cardiomyopathy;
 KW atherosclerosis; hypertension; congenital heart defect; aortic stenosis;
 KW atrial septal defect; atrioventricular canal defect; ductus arteriosus;
 KW pulmonary stenosis; subaortic stenosis; ventricular septal defect;
 KW valve disease; tuberculous sclerosis; scleroderma; obesity; transplantation;
 KW adrenoleukodystrophy; congenital adrenal hyperplasia; prostate cancer;
 KW neoplasm; adenocarcinoma; lymphoma; uterus cancer; fertility;
 KW haemophilia; hypercoagulation; idiopathic thrombocytopenic purpura;
 KW immunodeficiency; graft versus host disease; AIDS; bronchial asthma;
 KW Crohn's disease; G-coupled protein receptor; metabolic disorder;
 KW neurodegenerative disorder; receptor.
 XX OS
 XX Homo sapiens.
 XX PN
 XX US2004006205-A1.
 XX XX
 XX PD 08-JAN-2004.
 XX XX
 XX PF 02-APR-2002; 2002US-00115479.
 XX PR
 PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 30-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 XX (LILL/) LI L.
 PA (GERL/) GERLACH V.
 PA (LIUX/) LIU X.
 PA (MILL/) MILLER C E.
 PA (SPYT/) SPYTEK K A.
 PA (ZERH/) ZERHUSEN B D.
 PA (PENA/) PENA C E A.
 PA (SHEN/) SHENOV S G.
 PA (ZHON/) ZHONG H.
 PA (SMIT/) SMITHSON G.
 PA (CASM/) CASMAN S J.
 PA (BOLD/) BOLDOG F L.
 PA (VOSS/) VOSS E Z.
 PA (VERN/) VERNET C A.
 PA (MACD/) MACDOUGALL J R.
 PA (RAST/) RASTELLI L.
 PA (ANDE/) ANDERSON D W.
 PA (ZHON/) ZHONG M.
 PA (MEZE/) MEZES P S.
 PA (FURT/) FURTAK K.
 PA (PATI/) PATTURAJAN M.
 PA (BURG/) BURGESS C E.
 PA (MALY/) MALYANKAR U M.
 PA (SHIW/) SHIMKETS R A.

```

PA (TAUP/) TAUPIER R J.
PA (EDIN/) EDINGER S.
PA (MAZU/) MAZUR A.
XX
PI Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
PI Voss EZ, Vernat CM, Macdougall JR, Rastelli L, Anderson DW;
PI Mezes PS, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger S, Mazur A;
XX
DR WPI; 2004-224146/21.
DR N-PSDB; ADL93946.
XX
XX New G-coupled protein-receptor related polypeptides, for preventing
PT treating or ameliorating, e.g. acquired immunodeficiency syndrome,
PT bronchial asthma, Crohn's disease, prostate cancer, hemophilia,
PT scleroderma or obesity.
XX
PS Claim 1; Page 69; 220pp; English.
XX
CC The invention relates to isolated human G-coupled protein receptor-
CC related polypeptides and polynucleotides. The proteins are useful for
CC preventing, treating or ameliorating medical disorders by protein or gene
CC therapy. Disorders include cardiomyopathy, atherosclerosis, hypertension,
CC congenital heart defects, aortic stenosis, atrial septal defect,
CC subaortic stenosis, ventricular septal defect, valve diseases, tubercous
CC sclerosis, scleroderma, obesity, transplantation, adrenoleukodystrophy,
CC congenital adrenal hyperplasia, prostate cancer, neoplasm,
CC adenocarcinoma, lymphoma, uterus cancer, fertility, haemophilia,
CC hypercoagulation, idiopathic thrombocytopenic purpura,
CC immunodeficiencies, graft versus host disease, AIDS, bronchial asthma,
CC metabolic disorders, neurodegenerative disorders or Crohn's disease. They
CC are also useful as diagnostic or research tools. The present sequence
CC represents a human G-coupled protein receptor-related protein of the
CC invention.
XX
SQ Sequence 454 AA;

Query Match 73.6%; Score 226; DB 8; Length 454;
Best Local Similarity 72.7%; Pred. No. 6.3e-22;
Matches 40; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFGLNVTGKNEETLDMKKPRCGVPSGFGMLTPGNPKWERTNLTYSIRNY 55
DB 50 MQRFGLNVTGKNEETLDMKKPRCGVPSGFGMLTPGNPKWERTNLTYSIRNY 104

RESULT 12
ADE16002
ID ADE16002 standard; protein; 454 AA.
XX
AC ADE16002;
XX
XX 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID No 32.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nontropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipemic; neurodegenerative;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
XX WO200283841-A2.
XX
PD 24-OCT-2002.
XX
XX 03-APR-2002; 2002WO-US010713.
XX

```

Query Match

72.0%; Score 221; DB 7; Length 454;

Sequence 454 AA;

Best Local Similarity 70.9%; Pred. No. 3.1e-21; Mismatches 7; Indels 0; Gaps 0;
Matches 39; Conservative

QY 1 MQRFFGLNVTGKPNBETLDMKKPCRCVDPDGGFMLTPGNKWERNTLTVIRNY 55
DB 50 MQEFFGLKVTGKPDASTLKVMPKRCVDPDVAQFVLTEGNPRWEQHLTVIRNY 104

RESULT 13
ADE16004
ID ADE16004 standard; protein; 454 AA.
XX ADE16004;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID NO 34.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 05-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282334P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283710P.
PR 17-APR-2001; 2001US-0284234P.
PR 19-APR-2001; 2001US-0285325P.
PR 20-APR-2001; 2001US-0285609P.
PR 23-APR-2001; 2001US-0285748P.
PR 24-APR-2001; 2001US-0285890P.
PR 24-APR-2001; 2001US-0286068P.
PR 27-APR-2001; 2001US-0287213P.
PR 03-MAY-2001; 2001US-0288509P.
PR 30-MAY-2001; 2001US-0294495P.
PR 31-MAY-2001; 2001US-0294801P.
PR 31-JUL-2001; 2001US-0309216P.
PR 25-SEP-2001; 2001US-0324775P.
PR 28-NOV-2001; 2001US-0333900P.
PR 02-APR-2002; 2002US-00115479.
XX
PA (CURA-) CURAGEN CORP.
XX
XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
PI Pena CE, Shenoy SG, Zhong H, Smithson G, Caaman SJ, Boldog FL;
PI Voss EA, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
PI Zhong M, Mezes PD, Furtak X, Patturajan M, Burgess CE, Malyankar UM;
PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
XX
XX WPI; 2003-067574/06.
DR N-PSDB; ADE16003.
XX
XX New isolated NOVX polypeptides and polynucleotides, useful for
PT preventing, diagnosing or treating NOVX-associated disorders e.g.
PT diabetes, obesity, dyslipidaemias, cancer, Parkinson's disease,
PT Alzheimer's disease, infections.
XX
XX Claim 1; SEQ ID NO 34; 320pp; English.

XX The invention relates to a novel isolated G-coupled protein receptor
CC related polypeptides. The novel polypeptide comprise any of the 22 fully
CC defined sequences of 87-1780 amino acids, given in the specification;
CC their mature forms; and possible variants. The novel polypeptides have
CC the following activities: antidiabetic, anorectic, antibacterial,
CC virucide, fungicide, cytostatic, nootropic, neuroprotective,
CC antiparkinsonian, haemostatic, and antilipaemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
CC polypeptides of the invention.
XX
SQ Sequence 454 AA;
Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 3.1e-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKPNBETLDMKKPCRCVDPDGGFMLTPGNKWERNTLTVIRNY 55
DB 50 MQEFFGLKVTGKPDASTLKVMPKRCVDPDVAQFVLTEGNPRWEQHLTVIRNY 104

RESULT 14
ADE16008
ID ADE16008 standard; protein; 454 AA.
XX ADE16008;
XX
DT 29-JAN-2004 (first entry)
XX
DE G-coupled protein receptor related polypeptide, SEQ ID NO 38.
XX
KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
KW virucide; fungicide; cytostatic; nootropic; neuroprotective;
KW antiparkinsonian; haemostatic; antilipaemic; neurogenesis;
KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
KW preventive medicine; pharmacogenomics; human.
XX
OS Homo sapiens.
XX
PN WO200283841-A2.
XX
PD 24-OCT-2002.
XX
PF 03-APR-2002; 2002WO-US010713.
XX
PR 03-APR-2001; 2001US-0281136P.
PR 05-APR-2001; 2001US-0281863P.
PR 10-APR-2001; 2001US-0281906P.
PR 10-APR-2001; 2001US-0282334P.
PR 13-APR-2001; 2001US-0283657P.
PR 13-APR-2001; 2001US-0283678P.
PR 13-APR-2001; 2001US-0283687P.

PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0286068P.
 PR 24-APR-2001; 2001US-0286213P.
 PR 27-APR-2001; 2001US-0286590P.
 PR 30-MAY-2001; 2001US-0288509P.
 PR 31-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX (CURA-) CURAGEN CORP.
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16007.
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 FT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX Claim 1; SEQ ID NO 38; 320pp; English.
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.
 XX Sequence 454 AA;
 SQ Query Match 72.0%; Score 221; DB 7; Length 454;
 Best Local Similarity 70.9%; Pred. No. 3.1e-21;
 Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MQBFFGLVTKNEETLDMKKPCRCGVDPDGGCFMLTPGNPKWERTNLTIRYNY 55
 DB 50 MQBFFGLKVTGKPDATFLKVMKQPCRCGVDPDVAQFVLTEGPNRMEQTLTIRIENY 104

RESULT 15

ADE16006
 ID ADE16006 standard; protein; 454 AA.
 XX AC ADE16006;
 XX DT 29-JAN-2004 (first entry)
 XX DE G-coupled protein receptor related polypeptide, SEQ ID NO 36.
 XX KW G-coupled protein receptor; antidiabetic; anorectic; antibacterial;
 KW virucide; fungicide; cytostatic; neurotropic; neuroprotective;
 KW antiparkinsonian; haemostatic; antilipemic; neurogenesis;
 KW cell differentiation; cell proliferation; hematopoiesis; wound healing;
 KW angiogenesis; gene therapy; chromosome mapping; tissue typing;
 KW preventive medicine; pharmacogenomics; human.
 XX OS Homo sapiens.
 XX WO200283841-A2.
 XX PD 24-OCT-2002.
 XX PF 03-APR-2002; 2002WO-US010713.
 XX PR 03-APR-2001; 2001US-0281136P.
 PR 05-APR-2001; 2001US-0281863P.
 PR 05-APR-2001; 2001US-0281906P.
 PR 10-APR-2001; 2001US-0282934P.
 PR 13-APR-2001; 2001US-0283657P.
 PR 13-APR-2001; 2001US-0283678P.
 PR 13-APR-2001; 2001US-0283687P.
 PR 13-APR-2001; 2001US-0283710P.
 PR 17-APR-2001; 2001US-0284234P.
 PR 19-APR-2001; 2001US-0285325P.
 PR 20-APR-2001; 2001US-0285609P.
 PR 23-APR-2001; 2001US-0285748P.
 PR 23-APR-2001; 2001US-0285890P.
 PR 24-APR-2001; 2001US-0286068P.
 PR 27-APR-2001; 2001US-0287213P.
 PR 03-MAY-2001; 2001US-0288509P.
 PR 30-MAY-2001; 2001US-0294495P.
 PR 31-MAY-2001; 2001US-0294801P.
 PR 31-JUL-2001; 2001US-0309216P.
 PR 25-SEP-2001; 2001US-0324775P.
 PR 28-NOV-2001; 2001US-0333900P.
 PR 02-APR-2002; 2002US-00115479.
 XX (CURA-) CURAGEN CORP.
 XX Li L, Gerlach V, Liu X, Miller CE, Spytek KA, Zerhusen BD;
 PI Pena CEA, Shenoy SG, Zhong H, Smithson G, Casman SJ, Boldog FL;
 PI Voss EZ, Vernet CAM, Macdougall JR, Rastelli L, Anderson DW;
 PI Zhong M, Mezes PD, Furtak K, Patturajan M, Burgess CE, Malyankar UM;
 PI Shinkets RA, Taupier RJ, Edinger SR, Mazur A;
 XX WPI; 2003-067574/06.
 DR N-PSDB; ADE16005.
 XX New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders e.g.
 FT diabetes, obesity, dyslipidemias, cancer, Parkinson's disease,
 PT Alzheimer's disease, infections.
 XX Claim 1; SEQ ID NO 36; 320pp; English.
 XX The invention relates to a novel isolated G-coupled protein receptor
 CC related polypeptides. The novel polypeptide comprise any of the 22 fully
 CC defined sequences of 87-1780 amino acids, given in the specification;
 CC their mature forms; and possible variants. The novel polypeptides have
 CC the following activities: antidiabetic, anorectic, antibacterial,
 CC virucide, fungicide, cytostatic, neurotropic, neuroprotective,
 CC antiparkinsonian, haemostatic, and antilipemic. The G-coupled protein
 CC receptor related polypeptides are useful in a method of treating or
 CC preventing in a human, a pathology associated with the G-coupled protein
 CC receptor related polypeptides. The polypeptides are useful in the
 CC manufacture of a medicament for treating a syndrome associated with a
 CC human disease, preferably a NOVX-associated disorder. The novel
 CC polypeptides are useful for treating, preventing or diagnosing diseases,
 CC such as metabolic disorders, diabetes, obesity, infectious diseases,
 CC anorexia, cancer-associated diseases, neurodegenerative disorders,
 CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
 CC disorders, and various dyslipidemias, metabolic disturbances associated
 CC with obesity, metabolic X syndrome and wasting disorders associated with
 CC chronic diseases and various cancers. The nucleic acids and polypeptides
 CC may also be used as targets for the identification of small molecules
 CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
 CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
 CC therapy, in generation of antibodies that bind immunospecifically to NOVX
 CC substances for use in therapeutic or diagnostic methods. The nucleic
 CC acids are further used as hybridization probes, in chromosome mapping,
 CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
 CC represents one of the novel G-coupled protein receptor related
 CC polypeptides of the invention.

CC antiparkinsonian, haemostatic, and antilipaemic. The G-coupled protein
CC receptor related polypeptides are useful in a method of treating or
CC preventing in a human, a pathology associated with the G-coupled protein
CC receptor related polypeptides. The polypeptides are useful in the
CC manufacture of a medicament for treating a syndrome associated with a
CC human disease, preferably a NOVX-associated disorder. The novel
CC polypeptides are useful for treating, preventing or diagnosing diseases,
CC such as metabolic disorders, diabetes, obesity, infectious diseases,
CC anorexia, cancer-associated diseases, neurodegenerative disorders,
CC Alzheimer's disease, Parkinson's disease, immune disorders, hematopoietic
CC disorders, and various dyslipidaemias, metabolic disturbances associated
CC with obesity, metabolic X syndrome and wasting disorders associated with
CC chronic diseases and various cancers. The nucleic acids and polypeptides
CC may also be used as targets for the identification of small molecules
CC that modulate or inhibit e.g. neurogenesis, cell differentiation, cell
CC proliferation, hematopoiesis, wound healing and angiogenesis, in gene
CC therapy, in generation of antibodies that bind immunospecifically to NOVX
CC substances for use in therapeutic or diagnostic methods. The nucleic
CC acids are further used as hybridization probes, in chromosome mapping,
CC tissue typing, preventive medicine, and pharmacogenomics. This sequence
CC represents one of the novel G-coupled protein receptor related
XX polypeptides of the invention.

SQ Sequence 454 AA;

Query Match 72.0%; Score 221; DB 7; Length 454;
Best Local Similarity 70.9%; Pred. No. 3.le-21;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
QY 1 MQRFFGLNVTGKPEETLDMKKPRCGVDSGGFMLTPGNPKWERTNLTYSIRNY 55
DB 50 MQEFGGLKVTGKPDATLTKVMKQPRCGVDPVQAQFVLTEGNPRWEQHLTYRIENY 104

Search completed: May 27, 2005, 06:52:55
Job time : 106.827 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 20.8013 Seconds
(without alignments)
254.404 Million cell updates/sec

Title: US-10-032-376A-10
Perfect score: 307
Sequence: 1 MQRFFGLNVTGKPEETLDM.....LTPGNPKWERTNLTIRNY 55
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 KCHUN	neutrophil collage
2	233	75.9	468	1 KCRBI	interstitial colla
3	231	75.2	469	1 KCPGI	interstitial colla
4	221	72.0	469	1 KCHUI	interstitial colla
5	218	71.0	469	1 KCB0I	interstitial colla
6	201.5	65.6	384	2 I51267	collagenase (EC 3.
7	196	63.8	477	1 KCHUS1	stromelysin 1 (EC
8	195	63.5	476	1 KCHUS2	stromelysin 2 (EC
9	193	62.9	476	1 JC6505	stromelysin 1 (EC
10	193	62.9	477	1 KCMSS1	stromelysin 1 (EC
11	192	62.5	478	1 KCRBS1	stromelysin 1 (EC
12	190	61.9	476	1 KCRTS2	stromelysin 2 (EC
13	189	61.6	466	2 A23685	interstitial colla
14	189	61.6	472	2 S29243	interstitial colla
15	188	61.2	471	2 A53711	collagenase 3 (EC
16	188	61.2	475	1 KCRTHH	stromelysin 1 (EC
17	183	59.6	483	2 JC5743	matrix metalloprot
18	163	53.1	267	2 A57490	matrilysin (EC 3.4
19	160	52.1	267	1 KCHUM	matrilysin (EC 3.4
20	160	52.1	470	2 A49499	metalloelastase HM
21	160	52.1	663	1 S46492	gelatinase A (EC 3
22	155	50.5	662	2 S70365	gelatinase A (EC 3
23	153	49.8	660	1 A28153	gelatinase A (EC 3
24	153	49.8	662	2 A24296	gelatinase A (EC 3
25	153	49.8	662	2 S34780	gelatinase A (EC 3
26	139.5	45.4	669	2 I38029	matrix metalloprot
27	138	45.0	462	2 A42401	macrophage elastas
28	134.5	43.8	582	2 I38028	matrix metalloprot
29	134.5	43.8	582	2 I84471	matrix metalloprot

ALIGNMENTS

RESULT 1

KCHUN

neutrophil collagenase (EC 3.4.24.34) precursor [validated] - human

N/Alternate names: matrix metalloproteinase 8

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text change 09-Jul-2004

C/Accession: A37073; A61175; B61175; A36230; S09680; S11026; S19576; S27225; S32537; S62

R/Hasty, K.A.; Pourmotabbed, T.F.; Goldberg, G.I.; Thompson, J.P.; Spinella, D.G.; Steve

J. Biol. Chem. 265, 11421-11424, 1990

A/Title: Human neutrophil collagenase. A distinct gene product with homology to other ma

A/Reference number: A37073; MUID:90307647; PMID:2164002

A/Accession: A37073

A/Molecule type: mRNA

A/Residues: 1-467 <HNS>

A/Cross-references: UNIPROT:P22894; GB:J05556; NID:G180617; PIDN:AAA88021.1; PID:G180618

R/Devarajan, P.; Mookhtiar, K.; Van Wart, H.; Berliner, N.

Blood 77, 2731-2738, 1991

A/Title: Structure and expression of the cDNA encoding human neutrophil collagenase.

A/Reference number: A61175; MUID:91255696; PMID:1646048

A/Accession: A61175

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-31,'I',33-86,'E',88-467 <DEV>

A/Accession: B61175

A/Molecule type: protein

A/Residues: 263-264,'X',266-270,'X',272-273,'X',275,'X',277 <DE2>

R/Mallya, S.K.; Mookhtiar, K.A.; Gao, Y.; Brew, K.; Dioszegi, M.; Birkedal-Hansen, H.; V

Biochemistry 29, 10628-10634, 1990

A/Title: Characterization of 58-kilodalton human neutrophil collagenase: comparison with

A/Reference number: A36230; MUID:91104978; PMID:2176876

A/Accession: A36230

A/Molecule type: protein

A/Residues: 'X',86-87,'X',89-90,'X',92-97,'X',99-111,'X',113-120 <MAL>

R/Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 189, 295-300, 1990

A/Title: Characterization and activation of procollagenase from human polymorphonuclear

A/Reference number: S09680; MUID:90249372; PMID:2159879

A/Accession: S09680

A/Molecule type: protein

A/Residues: 21-31,'I',33-39,'I',41-47,'V',49-53,'I',55-72,'G',74-86,'E',88-111,'X',113-1

R/Knaeuper, V.; Kraemer, S.; Reinke, H.; Tschesche, H.

Biol. Chem. Hoppe-Seyler 371, 733, 1990

A/Title: Corrigendum. Partial amino-acid sequence of human PMN leukocyte procollagenase.

A/Reference number: S11026; MUID:91000455; PMID:2169766

A/Note: Original publication was Biol. Chem. Hoppe-Seyler 371 (Suppl.), 295-304, 1990

A/Accession: S11026

A/Molecule type: protein

A/Residues: 21-31,'I',33-53,'I',55-72,'G',74-111,'X',113-140:183-203,'X',205-209:248-261

A/Note: 87-Glu was also found

R/Blaeser, J.; Knaeuper, V.; Oethues, A.; Reinke, H.; Tschesche, H.

Eur. J. Biochem. 202, 1223-1230, 1991

RESULT 2
KCBI
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase; Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A27500; B27500; I46694
R;Finl, M.E.; Plucinska, I.M.; Mayer, A.S.; Grosse, R.H.; Brinckerhoff, C.E. Biochemistry 26, 6156-6165, 1987
A;Title: A gene for rabbit synovial cell collagenase: member of a family of metalloproteinases
A;Reference number: A27500; MUID:88077876; PMID:2825772
A;Accession: A27500
A;Molecule type: mRNA
A;Residues: 1-468 <PIN>
A;Cross-references: UNIPROT:P13943; GB:M19240
A;Accession: B27500
A;Molecule type: DNA
A;Residues: 1-391;399-468 <F12>
A;Cross-references: GB:M17820
A;Note: the location of the intron between exons 7 and 8 is approximate
R;Finl, M.E.; Austin, S.D.; Holt, P.T.; Ruby, P.L.; Gross, R.H.; White, H.D.; Brinckerhoff, C.E. Relat. Res. 6, 239-248, 1986
A;Title: Homology between exon-containing portions of rabbit genomic clones for synovial collagenase
A;Reference number: I46694; MUID:87029174; PMID:3021384
A;Accession: I46694
A;Status: translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 449-468 <F13>
A;Cross-references: GB:M25663; NID:G531211; PID:G531212
C;Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the triple helix. Procollagenase can be activated without removal of the activation peptide. Stimulation peptide by other proteinases
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are active
C;Genetics: 34/3; 116/2; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
A;Introns: 34/3; 116/2; 208/1; 260/1; 299/2; 344/1; 398/1; 433/1
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C;Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase; signal sequence #status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-468/Product: procollagenase #status predicted <PRO>
F;19-98/Domain: activation peptide #status predicted <ACT>
F;59-260/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;89-468/Product: interstitial collagenase #status predicted <MAT>
F;271-465/Domain: hemopexin repeat homology <PXN>
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;119,142/Binding site: carboxylate (Asn) (covalent) #status predicted
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status predicted
F;218/Active site: Glu #status predicted
F;277-465/Disulfide bonds: #status predicted

Query Match 75.9%; Score 233; DB 1; Length 468;
Best Local Similarity 74.5%; Pred. No. 1.6e-21;
Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
DB 66 MQEPPGLKVTGKPDATLKMKKPRCGVDPVAQFVLTFGNPRWEQTHLTIRNY 120

RESULT 3
KCPGI
Interstitial collagenase (EC 3.4.24.7) precursor [validated] - pig
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase; Sus scrofa domestica (domestic pig)
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: S15986; S13597
R;Richards, C.D.; Rafferty, J.A.; Reynolds, J.J.; Saklatvala, J. Matrix 11, 161-167, 1991
A;Title: Porcine collagenase from synovial fibroblasts: cDNA sequence and modulation of expression
A;Reference number: S15986; MUID:91333421; PMID:1651440
A;Accession: S15986

Query Match 100.0%; Score 307; DB 1; Length 467;
Best Local Similarity 100.0%; Pred. No. 6.7e-31;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 55
DB 66 MORFFGLNVTGKPNETLDMKKPRCGVDSGGFMLTGNPKWERTNLTIRNY 120

A;Title: Mercurial activation of human polymorphonuclear leucocyte procollagenase.
A;Reference number: S19576; MUID:92111500; PMID:1662606
A;Accession: S19576
A;Molecule type: protein
A;Residues: 69-103 <BL2>
R;Blaeser, J.; Triebel, S.; Reinke, H.; Tschesche, H. FEBS Lett. 313, 59-61, 1992
A;Title: Formation of a covalent Hg-Cys-bond during mercurial activation of PMNL procollagenase
A;Reference number: S27225; MUID:93050220; PMID:1330697
A;Accession: S27225
A;Molecule type: protein
A;Residues: 68-103 <BLA>
R;Knaeuper, V.; Osthus, A.; DeClercq, Y.A.; Langley, K.E.; Blaeser, J.; Tschesche, H. Biochem. J. 291, 847-854, 1993
A;Title: Fragmentation of human polymorphonuclear-leucocyte collagenase.
A;Reference number: S32527; MUID:93256897; PMID:8489511
A;Accession: S32527
A;Molecule type: protein
A;Residues: 100-112;263-276 <KN3>
R;Knaeuper, V.; Murphy, G.; Tschesche, H. Eur. J. Biochem. 235, 187-191, 1996
A;Title: Activation of human neutrophil procollagenase by stromelysin 2.
A;Reference number: S62608; MUID:96202934; PMID:8631328
A;Accession: S62608
A;Molecule type: protein
A;Residues: 21-39, 'I', 'V', 41-47, 'V', 49-122 <KN4>
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Rubin, B. submitted to the Brookhaven Protein Data Bank, January 1994
A;Reference number: A67078; PDB:1MNC
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 119-123, 1994
R;Stams, T.; Spurlino, J.C.; Smith, D.L.; Wahl, R.C.; Ho, T.F.; Qoronfleh, M.W.; Banks, Nat. Struct. Biol. 1, 119-123, 1994
A;Title: Structure of human neutrophil collagenase reveals large S1' specificity pocket.
A;Reference number: A58274; MUID:95384762; PMID:7656015
A;Contents: annotation; X-ray crystallography, 2.1 angstroms, residues 'G', 106-149, 'G', 119-123, 1994
C;Comment: This protein is more highly glycosylated than interstitial collagenase and is active
C;Genetics:
A;Gene: GDB:MMP8; CLG1
A;Cross-references: GDB:128173; OMIM:120355
A;Map position: 11q22.2-11q22.3
C;Function:
A;Description: hydrolyzes collagen types I, II, and III at Gly-Ile sites in collagenous A;Note: cleaves type I collagen most rapidly
A;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase; C;Keywords: calcium; extracellular matrix; glycoprotein; hydrolase; metalloproteinase; F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-467/Product: procollagenase #status predicted <PRO>
F;21-100/Domain: activation peptide #status experimental <ACT>
F;59-262/Domain: matrix metalloproteinase homology <MMP>
F;89-96/Region: autoinhibitory
F;101-467/Product: neutrophil collagenase #status predicted <MAT>
F;273-464/Domain: hemopexin repeat homology <PXN>
F;54,73,112,119,204,246/Binding site: carboxylate (Asn) (covalent) #status predicted
F;73-74/Cleavage site: Asn-Val (autolytic) #status experimental
F;84-85/Cleavage site: Asp-Met (autolytic) #status experimental
F;91,217,221,227/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status predicted
F;99-100/Cleavage site: Phe-Met (autolytic) #status experimental
F;167,169,182,195/Binding site: zinc, noncatalytic (His, Asp, His, His) #status experimental
F;174,175,177,179,200/Binding site: calcium (Asp, Gly, Asn, Ile, Asp, Glu) #status experimental
F;217,221,227/Binding site: zinc, catalytic (His) (active) #status experimental
F;218/Active site: Glu #status predicted
F;262-263/Cleavage site: Gly-Leu (autolytic) #status experimental
F;279-464/Disulfide bonds: #status predicted

A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-469 <RIC>
A;Cross-references: UNIPROT:P21692
A;Note: part of the sequence, including the amino end of the proenzyme, was confirmed by R;Clarke, N.J.; O'Hare, M.C.; Cawston, T.E.; Harper, G.P. Nucleic Acids Res. 18, 6703, 1990
A;Title: Nucleotide sequence of a cDNA for porcine type I collagenase, obtained by PCR.
A;Reference number: S13597; MUID:91067477; PMID:2174547
A;Accession: S13597
A;Molecule type: mRNA
A;Residues: 25-469 <CLA>
A;Cross-references: EMBL:X54724; NID:g2016; PIDN:CAA38526.1; PID:g930269
A;Li, J.; Brick, P.; Blow, D.M. submitted to the Brookhaven Protein Data Bank, April 1995
A;Reference number: A65568; PDB:1PBL
A;Contents: annotation; X-ray crystallography, 2.5 angstroms, residues 100-466
C;Comment: Procollagenase can be activated without removal of the activation peptide. Sc tion peptide by other proteinases.
C;Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which
C;Function:
A;Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and A;Note: also hydrolyzes type X collagen, serpins, and alpha-macroglobulins
C;Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotease
F;1-19/Domain: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloprotease
F;20-469/Product: signal sequence #status predicted <SIG>
F;20-99/Domain: procollagenase #status predicted <PRO>
F;60-261/Domain: activation peptide #status experimental <ACT>
F;100-469/Product: matrix metalloproteinase homology <MMP>
F;272-466/Domain: interstitial collagenase #status predicted <MAT>
F;92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;120,143/Binding site: zinc, catalytic (Asn) (covalent) #status predicted
F;218,222,228/Binding site: zinc, catalytic (His) (active) #status experimental
F;219/Active site: Glu #status predicted
F;278-466/Disulfide bonds: #status experimental

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 2.8e-21;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MQPFFGLNVTGKNNEETLDMKKPCRGVDSGGFMLTPGNKWTMLTVIRNY 55
||||| ||||| :|||:||||| :|||||:||||| :|||||
Db 67 MQPFFGLKVTGKPDAAETLVNKKPCRGVDSGGFMLTPGNRWENTHLYRIENY 121

RESULT 4
KCHUI
Interstitial collagenase (EC 3.4.24.7) precursor [validated] - human
N;Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence revision 30-Sep-1992 #text change 09-Jul-2004
C;Accession: A37308; S22766; I57620; A00996; D29157; A44518; S06132; B60964; S10595; S53
R;Templeton, N.S.; Brown, P.D.; Levy, A.T.; Margulies, I.M.K.; Liotta, L.A.; Stetler-St
Cancer Res. 50, 5431-5437, 1990
A;Title: Cloning and characterization of human tumor cell interstitial collagenase.
A;Reference number: A37308; MUID:90352587; PMID:2167156
A;Accession: A37308
A;Molecule type: mRNA
A;Residues: 1-469 <TEM>
A;Cross-references: UNIPROT:P03956; GB:X54925; NID:g30125; PIDN:CAA38691.1; PID:g30126
R;Brinckerhoff, C.E.; Ruby, P.L.; Austin, S.D.; Fini, M.E.; White, H.D.
J. Clin. Invest. 79, 542-546, 1987
A;Title: Molecular cloning of human synovial cell collagenase and selection of a single
A;Reference number: S22766; MUID:87105799; PMID:3027129
A;Accession: S22766
A;Molecule type: DNA
A;Residues: 1-63,65-70 <BRI>
A;Cross-references: EMBL:M15996; NID:g180666; PIDN:AAA35700.1; PID:g180667
R;Angel, P.; Baumann, I.; Stein, B.; Dellius, H.; Rahmsdorf, H.J.; Herrlich, P.
Mol. Cell. Biol. 7, 2256-2266, 1987
A;Title: 12-O-tetradecanoyl-phorbol-13-acetate induction of the human collagenase gene i
A;Reference number: I57620; MUID:87257941; PMID:3037355

A;Accession: I57620
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-35 <RES>
A;Cross-references: GB:M16567; NID:g180668; PIDN:AAA52033.1; PID:g180669
R;Goldberg, G.I.; Wilhelm, S.M.; Kronberger, A.; Bauer, E.A.; Grant, G.A.; Eisen, A.Z.
J. Biol. Chem. 261, 6600-6605, 1986
A;Title: Human fibroblast collagenase. Complete primary structure and homology to an onc
A;Reference number: A00996; MUID:86196089; PMID:3009463
A;Accession: A00996
A;Molecule type: mRNA
A;Residues: 1-114, 'R', '116-409, 'S', '411-469 <GOL>
A;Cross-references: GB:M13509; NID:g180664; PIDN:AAA35699.1; PID:g180665
A;Note: part of this sequence was confirmed by protein sequencing of the proenzyme
R;Whitham, S.E.; Murphy, G.; Angel, P.; Rahmsdorf, H.J.; Smith, B.J.; Lyons, A.; Harris
Biochem. J. 240, 913-916, 1986
A;Title: Comparison of human stromelysin and collagenase by cloning and sequence analysis
A;Reference number: A90336; MUID:87156645; PMID:3030290
A;Accession: D29157
A;Molecule type: mRNA
A;Residues: 1-199, 'H', '201-207, 'T', '209-469 <WHI>
A;Cross-references: EMBL:X05231; NID:g38266; PIDN:CAA28858.1; PID:g38267
A;Note: parts of this sequence, including the amino end of the proenzyme and of the matu
R;Birkedal-Hansen, B.; Moore, W.G.I.; Taylor, R.E.; Shown, A.S.; Birkedal-Hansen, H.
Biochemistry 27, 6751-6758, 1988
A;Title: Monoclonal antibodies to human fibroblast procollagenase. Inhibition of enzymat
end of the activated enzyme.
A;Reference number: A44518; MUID:89062403; PMID:2461732
A;Accession: A44518
A;Molecule type: protein
A;Residues: 270-305 <BIR>
R;Clark, I.M.; Cawston, T.E.
Biochem. J. 263, 201-206, 1989
A;Title: Fragments of human fibroblast collagenase. Purification and characterization.
A;Reference number: S06132; MUID:90104231; PMID:2557822
A;Accession: S06132
A;Status: preliminary
A;Molecule type: protein
A;Residues: 100-102, 'P', '104-107, 'XX', '110-112;270-277, 'X', '279-280, 'X', '282-287 <CLA>
R;Lark, M.W.; Walakovits, L.A.; Shah, T.K.; Vammiddlesworth, J.; Cameron, P.M.; Lin, T.Y.
Connect. Tissue Res. 25, 49-65, 1990
A;Title: Production and purification of prostromelysin and procollagenase from IL-1 beta
A;Reference number: A60964; MUID:91059606; PMID:2173990
A;Accession: B60964
A;Molecule type: protein
A;Residues: 24-35;100-108;270-272, 'X', '274, 'X', '276 <LAB>
R;Suzuki, K.; Nagase, H.; Ito, A.; Englund, J.J.; Salvesen, G.
Biol. Chem. Hoppe-Seyler 371(Suppl.), 305-310, 1990
A;Title: The role of matrix metalloproteinase 3 in the stepwise activation of human rheu
A;Reference number: S10595; MUID:90380300; PMID:2169257
A;Accession: S10595
A;Molecule type: protein
A;Residues: 20-102 <SUZ>
R;Suzuki, K.; Lees, M.; Newlands, G.F.J.; Nagase, H.; Woolley, D.E.
Biochem. J. 305, 301-306, 1995
A;Title: Activation of precursors for matrix metalloproteinases 1 (interstitial collagen
A;Reference number: S53438; MUID:95126921; PMID:7826345
A;Accession: S53438
A;Status: preliminary
A;Molecule type: protein
A;Residues: 20-108 <SUZ>
R;Springman, E.B.; Angleton, E.L.; Birkedal-Hansen, H.; Van Wart, H.E.
Proc. Natl. Acad. Sci. U.S.A. 87, 364-368, 1990
A;Title: Multiple modes of activation of latent human fibroblast collagenase: evidence f
A;Reference number: A44517; MUID:90115877; PMID:2153297
A;Contents: annotation; disulfide bond; activation mechanism
R;Salowe, S.P.; Marcy, A.I.; Cuca, G.C.; Smith, C.K.; Kopka, I.E.; Hagmann, W.K.; Hermes
Biochemistry 31, 4535-4540, 1992
A;Title: Characterization of zinc-binding sites in human stromelysin-1: stoichiometry of
A;Reference number: A43031; MUID:92256384; PMID:1591308
A;Contents: annotation; zinc ligand in proenzyme
A;Note: Cys-92 binds zinc in the proenzyme. Both active and proenzyme forms of the catal
C;Comment: Procollagenase can be activated without removal of the activation peptide. St

tion peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are secreted by fibroblasts.
C:Genetics:
A:Gene: GDB:MMP1; CLG
A:Cross-references: GDB:119783; OMIM:120353
A:Map position: 11q22.2-11q22.3
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-469/Product: procollagenase #status experimental <PRO>
F:20-99/Domain: activation peptide #status experimental <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status experimental <MAT>
F:172-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:120,143/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted
F:269-270/Cleavage site: Pro-life (autolytic) #status experimental
F:278-466/Disulfide bonds: #2:0%
Query Match 72.0% Score 221; DB 1; Length 469;
Best Local Similarity 70.9% Pred. No. 5.2e-20;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;
Qy 1 MQRPFGLVTKGNEETLDMKKPRCGVPSGGFMLTPGNKWERNTLVIRINY 55
Db 67 MQBFFGLKVGKPDATETLKVKOPRCGVPDVAQFVLTEGNPRWEQTHLTYRIENY 121
RESULT 5
KCB01
Interstitial collagenase (EC 3.4.24.7) precursor - bovine
N:Alternate names: fibroblast collagenase; matrix metalloproteinase 1 (MMP1); tissue collagenase
C:Species: Bos primigenius taurus (cattle)
C:Date: 30-Sep-1992 #sequence revision 30-Sep-1992 #text_change 09-Jul-2004
C:Accession: S14654; S20336; S14655
R:Tamura, M.; Shmookawa, H.; Sasaki, S.
submitted to the EMBL Data Library, March 1991
A:Reference number: S14654
A:Accession: S14654
A:Molecule type: mRNA
A:Residues: 1-469 <MAT>
A:Cross-references: UNIPROT:P28053; EMBL:X58256; NID:g259; PIDN:CAA41210.1; PID:g260
R:Sudbeck, B.D.; Jeffrey, J.J.; Weigus, H.G.; Mecham, R.P.; McCourt, D.; Parks, W.C.
Arch. Biochem. Biophys. 293, 370-376, 1992
A:Title: Purification and characterization of bovine interstitial collagenase and tissue collagenase
A:Reference number: S20336; MUID:92161820; PMID:1311165
A:Accession: S20336
A:Molecule type: protein
A:Residues: 19-21, 'FP', 24-29, 'L', 31-34, 'LL', 37-39, 'F', 86-105, 'NPR', 109-112, 'D', 114-125 <ACT>
C:Comment: This enzyme cleaves collagens of types I, II, and III at a Gly-Ile site in the activation peptide by other proteinases.
C:Comment: Procollagenase is found in glycosylated and unglycosylated forms, both of which are secreted by fibroblasts.
C:Function:
A:Description: hydrolyzes collagens, in particular types I, II, III, and X, serpins, and C:Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloproteinase C:Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metalloproteinase F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-469/Product: procollagenase #status predicted <PRO>
F:19-99/Domain: activation peptide #status predicted <ACT>
F:60-261/Domain: matrix metalloproteinase homology <MMP>
F:90-97/Region: autoinhibitory
F:100-469/Product: interstitial collagenase #status predicted <MAT>
F:172-466/Domain: hemopexin repeat homology <PXN>
F:92,218,222,228/Binding site: zinc, catalytic (Cys, His, His, His) (inhibited) #status predicted
F:120,143/Binding site: carboxydrate (Asn) (covalent) #status predicted
F:218,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F:219/Active site: Glu #status predicted

KCRTS2

stromelysin 2 (EC 3.4.24.22) precursor - rat
N/Alternate names: matrix metalloproteinase 10 (MMP10); transin-2
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1992 #sequence, revision 30-Sep-1992 #text_change 09-Jul-2004
C/Accession: B26403; A41775; S26498
R;Breathnach, R.; Matrisian, L.M.; Geanel, M.C.; Staub, A.; Leroy, P.
Nucleic Acids Res. 15, 1139-1151, 1987
A;/Title: Sequences coding for part of oncogene-induced transin are highly conserved in a
A;/Reference number: A26403; MUID:87146421; PMID:3547333
A;/Accession: B26403
A;/Molecule type: mRNA
A;/Residues: 1-476 <BRE>
A;/Cross-references: UNIPROT:P07152; EMBL:X05083; NID:G57388; PIDN:CAA28739.1; PID:G57389
A;/Note: Intron positions were determined by comparison of the cDNA sequence to genomic s
A;/Note: mRNA for this protein was expressed in several transformed rat embryo fibroblast
R;Chan, J.C.; Scanlon, M.; Zhang, H.Z.; Jia, L.B.; Yu, D.H.; Hung, M.C.; French, M.; Eas
J. Biol. Chem. 267, 1095-1103, 1992
A;/Title: Molecular cloning and characterization of v-mos-activated transformation-associ
A;/Reference number: A41775; MUID:92112748; PMID:1370458
A;/Accession: A41775
A;/Molecule type: mRNA
A;/Residues: 1-476 <CHA>
A;/Cross-references: GB:M65253; NID:G207150; PIDN:AAA42202.1; PID:G207151
A;/Note: sequence extracted from NCBI backbone (NCBIP:76184)
R;de Vouge, M.W.; Mukherjee, B.B.
Oncogene 7, 109-119, 1992
A;/Title: Transformation of normal rat kidney cells by v-K-ras enhances expression of tra
A;/Reference number: S26496; MUID:92158347; PMID:1741158
A;/Accession: S26498
A;/Status: preliminary; translation not shown
A;/Molecule type: mRNA
A;/Residues: 31-103,'L',241-242,'TOMESKPH',251,'L',253-254,'CE',293-294,'L',296 <DEV>
A;/Cross-references: EMBL:X64020
C:/Genetics:
A;/Introns: 35/3; 117/2; 167/1; 209/1; 264/1; 311/2; 356/1; 409/2; 444/1
C;/Superfamily: interstitial collagenase; hemopexin repeat homology; matrix metalloprotei
C;/Keywords: calcium; extracellular matrix; fibroblast; glycoprotein; hydrolase; metallo
F;/1-17/Domain: signal sequence #status predicted <SIG>
F;/18-476/Product: prostromelysin 2 #status predicted <PRO>
F;/18-99/Domain: activation peptide #status predicted <ACT>
F;/60-264/Domain: matrix metalloproteinase homology <MMP>
F;/90-97/Region: autoinhibitory
F;/100-476/Product: stromelysin 2 #status predicted <MAT>
F;/283-476/Domain: hemopexin repeat homology <PXN>
F;/92,218,222,228/Binding site: zinc, catalytic (Cys, His, His) (inhibited) #status
F;/120/Binding site: carboxylate (Asn) (covalent) #status predicted
F;/128,222,228/Binding site: zinc, catalytic (His) (active) #status predicted
F;/219/Active site: Glu #status predicted
F;/289-476/Disulfide bonds: #status predicted

Query Match 61.9%; Score 190; DB 1; Length 476;
Best Local Similarity 58.2%; Pred. No. 4.5e-16;
Matches 32; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTGKPEEETLDMWKPRCGVPDGGFMLTPGNPKWERTNLTVIRINY 55
|||:||||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Dd 67 MQKFGLGEMTGKLDNSTVENMMHKRCGPVDVGGFSTPFGSPKRWKHISYRINY 121

KEY
A23685

interstitial collagenase (EC 3.4.24.7) precursor - rat (fragment)
N/Alternate names: matrix metalloproteinase 1 (MMP1); vertebrate collagenase
C/Species: Rattus norvegicus (Norway rat)
C/Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 09-Jul-2004
C/Accession: A23685
R/Quinn, C.O.; Scott, D.K.; Brinckerhoff, C.E.; Matrisian, L.M.; Jeffrey, J.J.; Partridge, J. *Biol. Chem.* 265, 22342-22347, 1990
A/TITLE: Rat collagenase. Cloning, amino acid sequence comparison, and parathyroid hormone

C;Genetics:

C;Genetics:

A:Gene: GDB:MMP13; CLG3
A:Cross-references: GDB:373966; OMIM:600108
A:Map position: 11q22.2-11q22.3
C:Superfamily: interstitial collagenase; hemopexin repeat
C:Keywords: hydrolase; metalloproteinase; zinc; zymogen
F:64-267/Domain: matrix metalloproteinase homology <MMP>
F:278-471/Domain: hemopexin repeat homology <PN>
F:96,222,226,232/Binding site: zinc, catalytic (Cys, His, His, His)
F:222,226,232/Binding site: zinc, catalytic (His) (active) #status predicted
F:223/Active site: Glu #status predicted

Query Match 61.2%; Score 188; DB 2; Length 471;
Best Local Similarity 63.6%; Pred. No. 7.9e-16;
Matches 35; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MQRFFGLNVTKPNEETLDMKKPCRGVDPDSGGFMLTPGNPKWERTNLTYRINY 55
||| ||| ||| : ||| : ||| ||| ||| : ||| : ||| ||| |||
Db 71 MOSFFGLEVTGKLDDNTLDMKKPCRGVDPDGEYNTVFPTLLKWSKMLTYRINY 125

Search completed: May 27, 2005, 07:13:34
Job time : 20.8013 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 27, 2005, 06:46:16 ; Search time 96.25 Seconds
(without alignments)
292.617 Million cell updates/sec

Title: US-10-032-376A-10

Perfect score: 307

Sequence: 1 MQRFFGLNVTGKNEETLDM.....LTFGNPKWERTNLTIRINY 55

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	307	100.0	467	1 MM08_HUMAN	P22894 homo sapien
2	233	75.9	468	1 MM01_RABIT	P13943 oryctolagus
3	231	75.2	469	1 MM01_PIG	P21692 sus scrofa
4	223	72.5	466	1 MM08_RAT	O88766 rattus norv
5	222	72.3	469	1 MM01_HORSE	Q9XS25 equus cabal
6	221	72.0	469	1 MM01_HUMAN	P03956 homo sapien
7	218	71.0	469	1 MM01_BOVIN	P28053 bos taurus
8	201.5	65.6	384	1 MM01_RANCA	Q11133 rana catesb
9	198	64.5	465	2 O8C209	O8C209 mus musculu
10	198	64.5	465	2 O8C230	O8C230 mus musculu
11	198	64.5	478	2 Q6Y405	Q6Y405 canis fami
12	196	63.8	469	1 MM13_XENLA	Q10835 xenopus lae
13	196	63.8	472	2 Q93342	Q93342 gallus gall
14	196	63.8	472	2 Q10833	Q10833 xenopus lae
15	195	63.8	477	1 MM03_HUMAN	P08254 homo sapien
16	195	63.5	476	1 MM10_HUMAN	P09238 homo sapien
17	194	63.2	145	2 Q9N283	Q9N283 bos taurus
18	194	63.2	452	2 Q9TT82	Q9TT82 canis fami
19	193	62.9	476	1 MM10_MOUSE	O55123 mus musculu
20	193	62.9	477	1 MM03_MOUSE	P28862 mus musculu
21	193	62.9	479	2 Q922W6	Q922W6 mus musculu
22	192	62.5	478	1 MM03_RABIT	P28863 oryctolagus
23	190	61.9	465	1 MM08_MOUSE	O70138 mus musculu
24	190	61.9	476	1 MM10_RAT	P07152 rattus norv
25	189	61.6	466	1 MM13_RAT	P33435 mus musculu
26	189	61.6	472	1 MM13_MOUSE	P33435 mus musculu
27	188	61.2	383	2 Q7Z5M0	Q7Z5M0 homo sapien
28	188	61.2	393	2 Q8M1I8	Q8M1I8 felis silve
29	188	61.2	471	1 MM13_HUMAN	P45452 homo sapien
30	188	61.2	471	2 Q6NWN6	Q6NWN6 homo sapien
31	188	61.2	475	1 MM03_RAT	P03957 rattus norv

32 188 61.2 489 2 Q7Z5M1
33 187 60.9 472 1 MM13_HORSE
34 185 60.3 139 2 O9GM68
35 185 60.3 471 1 MM13_BOVIN
36 184 59.9 259 2 Q6DF35
37 184 59.9 481 1 MM20_BOVIN
38 183 59.6 471 2 Q98859
39 183 59.6 477 1 MM03_HORSE
40 183 59.6 483 1 MM20_HUMAN
41 183 59.6 483 1 MM20_PIG
42 183 59.6 483 2 O6DKT9
43 181 59.0 486 2 Q7SYX1
44 181 59.0 471 1 MM13_RABIT
45 179 58.3 482 1 MM20_MOUSE

Q7z5m1 homo sapien
O18927 equus cabal
O9gm68 sus scrofa
O77656 bos taurus
Q6df35 xenopus tro
O18767 bos taurus
Q98859 cynops pyrr
Q28397 equus cabal
O60882 homo sapien
P79287 sus scrofa
Q6dkr9 homo sapien
Q7syx1 xenopus lae
O62806 oryctolagus
P57748 mus musculu

ALIGNMENTS

RESULT 1

MM08_HUMAN STANDARD; PRT; 467 AA.
AC P22894;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8) (PMNL collagenase) (PMNL-CL).
GN Name=MMP8; Synonyms=CLG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 314-337; 347-363 AND 424-441.
RC TISSUE=Neutrophils;
RX MEDLINE=90307647; PubMed=2164002;
RA Hasty K.A., Pourmotabbed T.F., Goldberg G.I., Thompson J.P.,
RA Spinella D.G., Stevens R.M., Mainardi C.L.;
RT "Human neutrophil collagenase. A distinct gene product with homology
RT to other matrix metalloproteinases";
RL J. Biol. Chem. 265:11421-11424(1990).
RN [2]
RP SEQUENCE OF 21-140.
RC TISSUE=Neutrophils;
RX MEDLINE=90249372; PubMed=2159879;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Characterization and activation of procollagenase from human
RT polymorphonuclear leucocytes. N-terminal sequence determination of the
RT proenzyme and various proteolytically activated forms.";
RL Eur. J. Biochem. 189:295-300(1990).
RN [3]
RP SEQUENCE OF 21-103.
RC TISSUE=Neutrophils;
RX MEDLINE=92111500; PubMed=1662606;
RA Blaesser J., Knaeuper V., Osthus A., Reinke H., Tschesche H.;
RT "Mercurial activation of human polymorphonuclear leucocyte
RT procollagenase";
RL Eur. J. Biochem. 202:1223-1230(1991).
RN [4]
RP SEQUENCE OF 85-120, AND CHARACTERIZATION.
RC TISSUE=Neutrophils;
RX MEDLINE=91104978; PubMed=2176876;
RA Mallva S.K., Mookthiar K.A., Gao Y., Brew K., Dioszegi M.,
RA Birkedal-Hansen H., van Wart H.E.;
RT "Characterization of 58-kilodalton human neutrophil collagenase:
RT comparison with human fibroblast collagenase.";
RL Biochemistry 29:10628-10634(1990).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=90380298; PubMed=2169256;
RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
RT "Partial amino acid sequence of human PMN leukocyte procollagenase.";

RL Biol. Chem. Hoppe-Seyler 371:295-304(1990).
 RN [6]
 RP ERRATUM.
 RX MEDLINE=91000455; PubMed=2169766;
 RA Knaeuper V., Kraemer S., Reinke H., Tschesche H.;
 RL Biol. Chem. Hoppe-Seyler 371:733-733(1990).
 RN [7]
 RP Cysteine-Switch Mechanism.
 RX TISSUE=Neutrophils;
 RA MEDLINE=93050220; PubMed=1330697; DOI=10.1016/0014-5793(92)81184-N;
 RA Blaesser J., Triebel S., Reinke H., Tschesche H.;
 RT "Formation of a covalent Hg-Cys-bond during mercurial activation of
 RT PMNL procollagenase gives evidence of a cysteine-switch mechanism.";
 RL FEBS Lett. 313:59-61(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-262.
 RX MEDLINE=94185631; PubMed=8137810;
 RA Bode W., Reinemer P., Huber R., Klein T., Schnierer S., Tschesche H.;
 RT "The X-ray crystal structure of the catalytic domain of human
 RT neutrophil collagenase inhibited by a substrate analogue reveals the
 RT essentials for catalysis and specificity.";
 RL EMBO J. 13:1263-1269(1994).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-262.
 RX MEDLINE=94139930; PubMed=8307185; DOI=10.1016/0014-5793(94)80370-6;
 RA Reinemer P., Grams F., Huber R., Kleine T., Schnierer S., Piper M.,
 RA Tschesche H., Bode W.;
 RT "Structural implications for the role of the N terminus in the
 RT 'superactivation' of collagenases. A crystallographic study.";
 RL PDBS Lett. 338:227-233(1994).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 100-262.
 RX MEDLINE=95384762; PubMed=7656015;
 RA Stams T., Spurlino J.C., Smith D.L., Wahl R.C., Ho T.F.,
 RA Qoronfleh M.W., Banks T.M., Rubin B.;
 RT "Structure of human neutrophil collagenase reveals large S1'
 RT specificity pocket.";
 RL Nat. Struct. Biol. 1:119-123(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.81 ANGSTROMS) OF 100-262.
 RX MEDLINE=97390108; PubMed=9249047;
 RA Betz M., Huxley P., Davies S.J., Mushtaq Y., Pieper M., Tschesche H.,
 RA Bode W., Gomis-Rueth F.-X.;
 RT "1.8-A crystal structure of the catalytic domain of human neutrophil
 RT collagenase (matrix metalloproteinase-8) complexed with a
 RT peptidomimetic hydroxamate primed-side inhibitor with a distinct
 RT selectivity profile.";
 RL Eur. J. Biochem. 247:356-363(1997).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 105-262.
 RX MEDLINE=98318039; PubMed=9655333;
 RA Brandstätter H., Engl R.A., von Roeder E.G., Moroder L., Huber R.,
 RA Bode W., Grams F.;
 RT "Structure of malonic acid-based inhibitors bound to human neutrophil
 RT collagenase. A new binding mode explains apparently anomalous data.";
 RL Protein Sci. 7:1303-1309(1998).
 CC -I- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
 CC -I- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
 CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
 CC type III collagen more slowly than type I.
 CC -I- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit.
 CC -I- ENZYME REGULATION: Cannot be activated without removal of the
 CC activation peptide.
 CC -I- SUBCELLULAR LOCATION: Stored in intracellular granules.
 CC -I- TISSUE SPECIFICITY: Neutrophils.
 CC -I- SIMILARITY: Belongs to the peptidase M10A family.
 CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC -----
 CC EMBL; J05556; AAA88021.1; -.
 CC PIR; A37073; KCHUN.
 DR PDB; 1A85; X-ray; A=105-262.
 DR PDB; 1A86; X-ray; A=105-262.
 DR PDB; 1B28; X-ray; A=99-263.
 DR PDB; 1173; X-ray; A=100-262.
 DR PDB; 1176; X-ray; A=100-262.
 DR PDB; 1JAN; X-ray; A=99-262.
 DR PDB; 1JAO; X-ray; A=100-262.
 DR PDB; 1JAP; X-ray; A=100-262.
 DR PDB; 1JQA; X-ray; A=100-262.
 DR PDB; 1JHI; X-ray; A=105-262.
 DR PDB; 1JJI; X-ray; A=100-262.
 DR PDB; 1KBC; X-ray; A/B=99-262.
 DR PDB; 1MWB; X-ray; A=100-262.
 DR PDB; 1MNC; X-ray; @=101-263.
 DR MEROPS; M10.002; -.
 DR Genew; HGNC:7175; MMP8.
 DR MIM; 120355; -.
 DR GO; GO:0005615; C:extracellular space; TAS.
 DR GO; GO:0008130; F:neutrophil collagenase activity; TAS.
 DR GO; GO:0008270; F:zinc ion binding; TAS.
 DR GO; GO:0005508; P:proteolysis and peptidolysis; TAS.
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR009070; PGSD-like.
 DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF00413; Peptidase_M10; 1.
 DR Pfam; PF03933; Peptidase_M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC PROTEASE; 1.
 DR 3D-structure; Calcium-Binding; Collagen degradation;
 KW Direct protein sequencing; Extracellular matrix; Glycoprotein;
 KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
 FT SIGNAL 1 20
 FT PROPEP 21 100 Activation peptide.
 FT CHAIN 101 467 Neutrophil collagenase.
 FT DOMAIN 276 467 Hemopexin-like.
 FT SITE 91 91 Cysteine switch.
 FT METAL 157 157 Calcium 1.
 FT METAL 167 167 Zinc 1.
 FT METAL 169 169 Zinc 1.
 FT METAL 174 174 Calcium 2.
 FT METAL 175 175 Calcium 2 (via carbonyl oxygen).
 FT METAL 177 177 Calcium 2 (via carbonyl oxygen).
 FT METAL 179 179 Calcium 2 (via carbonyl oxygen).
 FT METAL 182 182 Zinc 1.
 FT METAL 189 189 Calcium 1 (via carbonyl oxygen).
 FT METAL 191 191 Calcium 1 (via carbonyl oxygen).
 FT METAL 193 193 Calcium 1.
 FT METAL 195 195 Zinc 1.
 FT METAL 197 197 Calcium 2.
 FT METAL 200 200 Calcium 2.
 FT METAL 217 217 Zinc 2 (catalytic).
 FT ACT_SITE 218 218 Zinc 2 (catalytic).
 FT METAL 221 221 Zinc 2 (catalytic).
 FT METAL 227 227 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 286 similarity).
 FT METAL 378 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 425 similarity).
 FT METAL 54 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 73 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 112 N-linked (GlcNAc...) (Probable).
 FT CARBOHYD 204 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 246 246 N-linked (GlcNAc...) (Potential).
 FT DISULFID 279 464 Probable.

Query Match 100.0%; Score 307; DB 1; Length 467;
 Best Local Similarity 100.0%; Pred. No. 2.6e-29; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMTFGNPKWERTNLTIRYNY 55
 |||||
 Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMTFGNPKWERTNLTIRYNY 120
 |||||

RESULT 2

MM01_RABIT STANDARD; PRT; 468 AA.
 AC PI3943;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
 DE metalloproteinase-1) (MMP-1).
 GN Name=MMP1;
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=88077876; PubMed=2825772;
 RA Fini M.E., Plucinska I.M., Mayer A.S., Gross R.H., Brinckerhoff C.E.;
 RT "A gene for rabbit synovial cell collagenase: member of a family of
 RT metalloproteinases that degrade the connective tissue matrix.";
 RL Biochemistry 26:6156-6165(1987).
 RN [2]
 RP SEQUENCE OF 449-468 FROM N.A.
 RC STRAIN=New Zealand white;
 RX MEDLINE=87029174; PubMed=3021384;
 RA Fini M.E., Austin S.D., Holt P.T., Ruby P.L., Gross R.H., White H.D.,
 RA Brinckerhoff C.E.;
 RT "Homology between exon-containing portions of rabbit genomic clones
 RT for synovial cell collagenase and human foreskin and synovial cell
 RT mRNAs.";
 RL Coll. Relat. Res. 6:239-248(1986).

CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-I-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where P1' is a
 CC hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
 CC similarity).
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.

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CC EMBL; M17823; AAB88016.1; -
 CC EMBL; M17820; AAB88016.1; JOINED.
 CC EMBL; M17821; AAB88016.1; JOINED.
 CC EMBL; M17822; AAB88016.1; JOINED.
 CC EMBL; M19240; AAB88016.1; JOINED.
 CC EMBL; M25663; AAA31203.1; -

DR PIR; A27500; KCRBI.
 DR HSSP; P03956; 1CGL.
 DR MEROPS; M10.001; -
 DR InterPro; IPR000585; Hemopexin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR006026; Peptidase_M.
 DR InterPro; IPR009070; PGBD like.
 DR Pfam; PF00413; Hemopexin; 4.
 DR Pfam; PF00445; Hemopexin; 4.
 DR Pfam; PF03933; Peptidase_M10; 1.
 DR PRINTS; PR00138; Peptidase_M10_N; 1.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; ZnMc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Calcium-binding; Collagen degradation; Extracellular matrix;
 KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
 KW Zymogen.
 FT SIGNAL 1 18 Activation peptide.
 FT PROPEP 19 98 Interstitial collagenase.
 FT CHAIN 99 468 Hemopexin-like.
 FT DOMAIN 274 468 Cysteine switch (Potential).
 FT SITE 91 91 Calcium 1 (By similarity).
 FT METAL 123 123 Calcium 2 (By similarity).
 FT METAL 157 157 Zinc 1 (By similarity).
 FT METAL 167 167 Zinc 1 (By similarity).
 FT METAL 169 169 Calcium 3 (By similarity).
 FT METAL 174 174 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 175 175 similarity).
 FT METAL 177 177 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 179 179 similarity).
 FT METAL 182 182 Calcium 3 (via carbonyl oxygen) (By
 FT METAL 189 189 similarity).
 FT METAL 191 191 Calcium 2 (via carbonyl oxygen) (By
 FT METAL 193 193 similarity).
 FT METAL 195 195 Calcium 2 (By similarity).
 FT METAL 197 197 Zinc 1 (By similarity).
 FT METAL 198 198 Calcium 3 (By similarity).
 FT METAL 200 200 Calcium 1 (By similarity).
 FT METAL 217 217 Calcium 3 (By similarity).
 FT ACT_SITE 218 217 Zinc 2 (catalytic) (By similarity).
 FT METAL 221 221 By similarity.
 FT METAL 227 227 Zinc 2 (catalytic) (By similarity).
 FT METAL 284 284 Zinc 2 (catalytic) (By similarity).
 FT METAL 328 328 Calcium 4 (via carbonyl oxygen) (By
 FT METAL 377 377 similarity).
 FT METAL 426 426 Calcium 4 (via carbonyl oxygen) (By
 FT METAL 465 465 similarity).
 FT CARBOHYD 119 119 Calcium 4 (via carbonyl oxygen) (By
 FT DISULFID 277 465 N-linked (GlcNAc...) (Probable).
 SQ SEQUENCE 468 AA; 53739 MW; DA9053891952B8C CRC64;

Query Match 75.9%; Score 233; DB 1; Length 468;
 Best Local Similarity 74.5%; Pred. No. 3.7e-20;
 Matches 41; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMTFGNPKWERTNLTIRYNY 55
 |||||
 Db 66 MORFFGLNVTGKNEETLDMKKPCGVPDGGFMTFGNPKWERTNLTIRYNY 120
 |||||

RESULT 3
 MM01_PIG

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ID AC MM01_PIG STANDARD; PRT; 469 AA.
DT P21692;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Name:MMP1;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91333421; PubMed=1651440;
RA Richards C.D., Rafferty J.A., Reynolds J.J., Saklatvala J.;
RT "Porcine collagenase from synovial fibroblasts: cDNA sequence and
RT modulation of expression of RNA in vitro by various cytokines.";
RL Matrix 11:161-167(1991).
RN [2]
RP SEQUENCE OF 25-469 FROM N.A.
RX TISSUE=Synovial cell;
RX MEDLINE=91067477; PubMed=2174547;
RA Clarke N.J., O'Hare M.C., Cawston T.E., Harper G.P.;
RT "Nucleotide sequence of a cDNA for porcine type I collagenase,
RT obtained by PCR.";
RL Nucleic Acids Res. 18:6703-6703(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 100-469.
RX MEDLINE=96173003; PubMed=8590015; DOI=10.1016/S0969-2126(01)00188-5;
RA Li J., Brick P., O'Hare M.C., Skarzynski T., Lloyd L.F., Curry V.A.,
RA Clark I.M., Bigg H.F., Hazleman B.L., Cawston T.E., Blow D.M.;
RT "Structure of full-length porcine synovial collagenase reveals a C-
RT terminal domain containing a calcium-linked, four-bladed beta-
RT propeller.";
RL Structure 3:541-549(1995).
RN [4]
RP SEQUENCE OF 100-104 AND 248-282, AND AUTOPROTEOLYTIC CLEAVAGE SITE.
RX MEDLINE=95142635; PubMed=7840605; DOI=10.1006/abbi.1995.1018;
RA Clark I.M., Mitchell R.E., Powell L.K., Bigg H.F., Cawston T.E.,
RA O'Hare M.C.;
RT "Recombinant porcine collagenase: purification and autolysis.";
RL Arch. Biochem. Biophys. 316:123-127(1995).
CC -I- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -I- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -I- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
CC -I- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -I- PTM: Undergoes autocatalytic cleavage to produce a N-terminal fragment
CC having reduced collagenolytic activity.
CC -I- SIMILARITY: Belongs to the peptidase M10A family.
CC -I- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54724; CAA38526.1; -
DR PIR; S15986; KCPGI.
DR PDB; 1FBL; X-ray; @=100-469.
DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.

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DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZNMC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW 3D-structure; Autocatalytic cleavage; Calcium-binding;
KW Collagen degradation; Direct protein sequencing; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 19 Activation peptide.
FT PROPEP 20 99 Interstitial collagenase.
FT CHAIN 100 469 18 kDa interstitial collagenase.
FT CHAIN 100 258 Hemopexin-like.
FT DOMAIN 275 469 Cysteine switch (Potential).
FT SITE 92 92 Cleavage (autolytic).
FT SITE 258 259 Calcium 1.
FT METAL 124 124 Calcium 2.
FT METAL 158 158 Calcium 1.
FT METAL 168 168 Zinc 1.
FT METAL 170 170 Zinc 1.
FT METAL 175 175 Calcium 3.
FT METAL 176 176 Calcium 3 (via carbonyl oxygen).
FT METAL 178 178 Calcium 3 (via carbonyl oxygen).
FT METAL 180 180 Calcium 3 (via carbonyl oxygen).
FT METAL 183 183 Zinc 1.
FT METAL 190 190 Calcium 2 (via carbonyl oxygen).
FT METAL 192 192 Calcium 2 (via carbonyl oxygen).
FT METAL 194 194 Calcium 2.
FT METAL 196 196 Zinc 1.
FT METAL 198 198 Calcium 3.
FT METAL 199 199 Calcium 1.
FT METAL 201 201 Calcium 3.
FT METAL 218 218 Zinc 2 (catalytic).
FT ACT_SITE 219 219 Zinc 2 (catalytic).
FT METAL 222 222 Zinc 2 (catalytic).
FT METAL 228 228 Calcium 4 (via carbonyl oxygen).
FT METAL 285 285 Calcium 4 (via carbonyl oxygen).
FT METAL 329 329 Calcium 4 (via carbonyl oxygen).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen).
FT DISULFID 278 466 N-linked (GlcNAc..)(Potential).
FT CARBOHYD 120 120
FT STRAND 101 102
FT TURN 104 105
FT STRAND 113 118
FT TURN 123 124
FT TURN 127 142
FT TURN 143 144
FT STRAND 148 152
FT STRAND 159 164
FT STRAND 182 184
FT TURN 190 193
FT STRAND 195 198
FT TURN 199 200
FT STRAND 204 204
FT STRAND 211 211
FT HELIX 212 223
FT TURN 224 225
FT STRAND 226 227
FT TURN 232 233
FT TURN 235 236
FT HELIX 250 260
FT TURN 277 278
FT TURN 280 281
FT TURN 286 290
FT TURN 291 292

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FT STRAND 293 298
FT TURN 299 300
FT STRAND 301 305
FT STRAND 313 316
FT HELIX 317 320
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 344
FT TURN 345 346
FT STRAND 347 352
FT TURN 353 354
FT STRAND 355 356
FT TURN 358 359
FT STRAND 362 363
FT HELIX 364 368
FT TURN 372 373
FT STRAND 379 383
FT TURN 384 387
FT STRAND 388 393
FT TURN 394 395
FT STRAND 396 401
FT TURN 402 405
FT STRAND 406 407
FT STRAND 413 414
FT HELIX 415 418
FT TURN 420 421
FT STRAND 428 432
FT TURN 433 434
FT STRAND 435 440
FT TURN 441 442
FT STRAND 443 448
FT TURN 449 452
FT STRAND 453 459
FT TURN 460 461
FT HELIX 462 464
FT TURN 465 465
SQ SEQUENCE 469 AA; 53666 MM; 7952D72B2753F682 CRC64;

Query Match 75.2%; Score 231; DB 1; Length 469;
Best Local Similarity 72.7%; Pred. No. 6.5e-20;
Matches 40; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

QY 1 MQRPFGLVNTGKPNETLDMKKPCGVPDSGGFMLTPGNPKWERTNLTYYRINY 55
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 67 MQQFGLKVTGKPDATLNMVKPCGVPDVAEFLTPGNPRWENTHLYRIENY 121

RESULT 4
MM08_RAT
ID MM08_RAT STANDARD; PRT; 466 AA.
AC O88766;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neutrophil collagenase precursor (EC 3.4.24.34) (Matrix
DE metalloproteinase-8) (MMP-8).
GN Name=Mmp8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Lewis;
RA Overall C.M., Lowe D., Wells G., Clements J.M.;
RT "Cloning, expression, characterization and activation properties of
RT rat neutrophil collagenase (MMP-8).";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Can degrade fibrillar type I, II, and III collagens.
CC -!- CATALYTIC ACTIVITY: Cleavage of interstitial collagens in the
CC triple helical domain. Unlike EC 3.4.24.7, this enzyme cleaves
CC type III collagen more slowly than type I.
CC -!- COFACTOR: Binds 2 zinc ions and 3 calcium ions per subunit (By

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similarity).
CC -!- ENZYME REGULATION: Cannot be activated without removal of the
CC activation peptide (By similarity).
CC -!- SUBCELLULAR LOCATION: Stored in intracellular granules.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/ebis/
CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL; AJ007288; CAA07432.1; -.
CC HSSP; P22894; 1BZS.
CC MEROPS; M10.002; -.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR009070; PGED_like.
CC Pfam; PF00045; Hemopexin; 4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC PRINTS; PR00138; MATRIXIN.
CC PROSITE; PS00546; CYSTEINE_SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT SIGNAL 1 20 By similarity.
FT PROPEP 21 101 Activation peptide (By similarity).
FT CHAIN 102 466 Neutrophil collagenase.
FT DOMAIN 277 466 Hemopexin-like.
FT SITE 92 92 Cysteine switch (By similarity).
FT METAL 158 158 Calcium 1 (By similarity).
FT METAL 168 168 Zinc 1 (By similarity).
FT METAL 170 170 Zinc 1 (By similarity).
FT METAL 175 175 Calcium 2 (By similarity).
FT METAL 176 176 Calcium 2 (via carbonyl oxygen) (By
FT METAL 178 178 similarity).
FT METAL 180 180 Calcium 2 (via carbonyl oxygen) (By
FT METAL 183 183 similarity).
FT METAL 190 190 Calcium 2 (via carbonyl oxygen) (By
FT METAL 192 192 similarity).
FT METAL 194 194 Calcium 1 (By similarity).
FT METAL 196 196 Zinc 1 (By similarity).
FT METAL 198 198 Calcium 2 (By similarity).
FT METAL 201 201 Calcium 2 (By similarity).
FT METAL 218 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 219 By similarity.
FT METAL 222 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 228 Zinc 2 (catalytic) (By similarity).
FT METAL 287 287 Calcium 3 (via carbonyl oxygen) (By
FT METAL 379 379 similarity).
FT METAL 426 426 Calcium 3 (via carbonyl oxygen) (By
FT METAL 465 465 similarity).
FT DISULFID 280 465 Probable.
FT CARBOHYD 56 56 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 113 113 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 466 AA; 53277 MW; 8B9DE97576E76C90 CRC64;

Query Match 72.6%; Score 223; DB 1; Length 466;
Best Local Similarity 70.9%; Pred. No. 6.3e-19;

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Matches 39; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 1 MQRFFGLVNTGKPNSETLDMKKPCGVPDSCGGFMLTGCNPKWERTNLTIRNY 55
    ||||| ||||| : : : : ||||| : : : : ||||| : : : : ||||| :
Db 67 MQRFFGLPTGKPDAAITIMEKPCGVPDSCGGFLLTSPGPKWTHNLTIRNIH 121
    ||||| ||||| : : : : ||||| : : : : ||||| : : : : ||||| :

RESULT 5
MM01_HUMAN
ID MM01_HUMAN STANDARD; PRT; 469 AA.
AC Q9X3Z5;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1).
GN Names=MMP1;
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]_
RP SEQUENCE FROM N.A.
RA Richardson D.W.;
RT "Cloning and expression of equine matrix metalloproteinase 1
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagen of types VII and X.
CC -!- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where p1' is a
CC hydrophobic residue.
CC -!- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -!- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide.
CC -!- SIMILARITY: Belongs to the peptidase M10A family.
CC -!- SIMILARITY: Contains 1 hemopexin-like domain.
CC
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CC
CC -----
CC EMBL; AF148882; AAD38030.1; -.
CC HSP; P03956; 1AYK.
CC
CC DR MEROPS; M10_001; -.
CC InterPro; IPR000585; Hemopexin.
CC InterPro; IPR001818; Pept_M10A_M12B.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR006026; Peptidase_M.
CC InterPro; IPR009070; PGD like.
CC Pfam; PF00045; Hemopexin_4.
CC Pfam; PF00413; Peptidase_M10; 1.
CC Pfam; PF03933; Peptidase_M10_N; 1.
CC PRINTS; PR00138; MATRIXIN.
CC SMART; SM00120; HX; 4.
CC SMART; SM00235; ZnMc; 1.
CC PROSITE; PS00546; CYSTEINE SWITCH; 1.
CC PROSITE; PS00024; HEMOPEXIN; 1.
CC PROSITE; PS00142; ZINC_PROTEASE; 1.
CC Calcium-binding; Collagen degradation; Extracellular matrix;
CC Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
CC Zymogen.
KW SIGNAL.
FT PROPEP 1 18 By similarity.
FT CHAIN 19 99 Activation peptide.
FT 100 469 Interstitial collagenase.
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FT DOMAIN 275 469 Hemopexin-like.
FT SITE 92 Cysteine switch (Potential).
FT METAL 124 Calcium 1 (By similarity).
FT METAL 158 Calcium 2 (By similarity).
FT METAL 168 Zinc 1 (By similarity).
FT METAL 170 Zinc 1 (By similarity).
FT METAL 176 Calcium 3 (By similarity).
FT METAL 176 Calcium 3 (via carbonyl oxygen) (By
FT METAL 178 similarity).
FT METAL 178 Calcium 3 (via carbonyl oxygen) (By
FT METAL 180 similarity).
FT METAL 180 Calcium 3 (via carbonyl oxygen) (By
FT METAL 183 similarity).
FT METAL 190 Zinc 1 (By similarity).
FT METAL 190 Calcium 2 (via carbonyl oxygen) (By
FT METAL 192 similarity).
FT METAL 192 Calcium 2 (via carbonyl oxygen) (By
FT METAL 194 similarity).
FT METAL 194 Calcium 2 (By similarity).
FT METAL 196 Zinc 1 (By similarity).
FT METAL 198 Calcium 3 (By similarity).
FT METAL 199 Calcium 1 (By similarity).
FT METAL 201 Calcium 3 (By similarity).
FT METAL 218 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 219 By similarity.
FT METAL 222 Zinc 2 (catalytic) (By similarity).
FT METAL 228 Zinc 2 (catalytic) (By similarity).
FT METAL 285 Calcium 4 (via carbonyl oxygen) (By
FT METAL 329 similarity).
FT METAL 329 Calcium 4 (via carbonyl oxygen) (By
FT METAL 378 similarity).
FT METAL 427 Calcium 4 (via carbonyl oxygen) (By
FT DISULFID 278 By similarity.
FT SEQUENCE 469 AA; 54001 MW; AE86760AB2C529CA CRC64;

Query Match 72.3%; Score 222; DB 1; Length 469;
Best Local Similarity 70.9%; Pred. No. 8.4e-19;
Matches 39; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

QY 1 MQRFFGLVNTGKPNSETLDMKKPCGVPDSCGGFMLTGCNPKWERTNLTIRNY 55
Db 67 MQRFFGLPTGKPDAAITIMEKPCGVPDSCGGFLLTSPGPKWTHNLTIRNIY 121

RESULT 6
MM01_HUMAN
ID MM01_HUMAN STANDARD; PRT; 469 AA.
AC P03956; P08156;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (Fibroblast collagenase).
GN Name=MMP1; Synonyms=CLG;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A.
RX MEDLINE=90352587; PubMed=2167156;
RA Templeton N.S., Brown P.D., Levy A.T., Margulies I.M.K., Liotta L.A.,
RA Stetler-Stevenson W.G.;
RT "Cloning and characterization of human tumor cell interstitial
RT collagenase."
RL Cancer Res. 50:5431-5437(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87156645; PubMed=3030290;
RA Whitham S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
```

RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
 RT "Comparison of human stromelysin and collagenase by cloning and
 RT sequence analysis.";
 RL Biochem. J. 240:913-916(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86196089; PubMed=3009463;
 RA Goldberg G.I., Wilhelm S.M., Kronberger A., Bauer E.A., Grant G.A.,
 RA Eisen A.Z.;
 RT "Human fibroblast collagenase. Complete primary structure and homology
 RT to an oncogene transformation-induced rat protein.";
 RL J. Biol. Chem. 261:6600-6605(1986).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
 RA Chung E., Davis K., Federpiel N., Hyman R., Kalman S., Komp C.,
 RA Kurdil O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
 RA Heller R., Davis R.W.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J.J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE OF 1-35 FROM N.A.
 RX MEDLINE=87257941; PubMed=3037355;
 RA Angel P., Baumann I., Stein B., Delius H., Rahmsdorf H.J.,
 RA Herrlich P.;
 RT "12-O-tetradecanoyl-phorbol-13-acetate induction of the human
 RT collagenase gene is mediated by an inducible enhancer element located
 RT in the 5'-flanking region.";
 RL Mol. Cell. Biol. 7:2256-2266(1987).
 RN [7]
 RP SEQUENCE OF 1-70 FROM N.A.
 RC TISSUE=Synovial cell;
 RX MEDLINE=87109799; PubMed=3027129;
 RA Brinckerhoff C.E., Ruby P.L., Austin S.D., Fini M.E., White H.D.;
 RT "Molecular cloning of human synovial cell collagenase and selection of
 RT a single gene from genomic DNA.";
 RL J. Clin. Invest. 79:542-546(1987).
 RN [8]
 RP SEQUENCE OF 100-112 AND 270-287.
 RC TISSUE=Fibroblast;
 RX MEDLINE=90104231; PubMed=2557822;
 RA Clark I.M., Cawston T.E.;
 RT "Fragments of human fibroblast collagenase. Purification and
 RT characterization.";
 RL Biochem. J. 263:201-206(1989).
 RN [9]
 RP SIMILARITY TO THERMOLYSIN TYPE PROTEASES.
 RX MEDLINE=87194799; PubMed=3032950;
 RA McKerrow J.H.;
 RT "Human fibroblast collagenase contains an amino acid sequence
 homologous to the zinc-binding site of Serratia protease.";
 RL J. Biol. Chem. 262:5943-5943(1987).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 100-269.
 RX MEDLINE=95384760; PubMed=7656013;
 RA Borkakoti N., Winkler F.K., Williams D.H., D'Arcy A., Broadhurst M.J.,
 RA Brown P.A., Johnson W.H., Murray E.J.;
 RT "Structure of the catalytic domain of human fibroblast collagenase
 RT complexed with an inhibitor.";
 RL Nat. Struct. Biol. 1:106-110(1994).
 RN [11]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 102-269.
 RX MEDLINE=94304829; PubMed=8031754;
 RA Lovejoy B., Hassell A.M., Luther M.A., Weigl D., Jordan S.R.;
 RT "Crystall structures of recombinant 19-kDa human fibroblast collagenase
 RT complexed to itself.";
 RL Biochemistry 33:8207-8217(1994).
 RN [12]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 102-269.
 RX MEDLINE=94105765; PubMed=8278810;
 RA Lovejoy B., Cleasby A., Hassell A.M., Longley K., Luther M.A.,
 RA Weigl D., McGeehan G., McElroy A.B., Drewry D., Lambert M.H.,
 RA Jordan S.R.;
 RT "Structure of the catalytic domain of fibroblast collagenase complexed
 RT with an inhibitor.";
 RL Science 263:375-377(1994).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (1.56 ANGSTROMS) OF 101-269.
 RX MEDLINE=94377426; PubMed=8090713;
 RA Spurlino J.C., Smallwood A.M., Carlton D.D., Banks T.M., Vavra K.J.,
 RA Johnson J.S., Cook E.R., Falvo J., Wahl R.C., Pulvino T.A., Et A.L.;
 RT "1.56-A structure of mature truncated human fibroblast collagenase.";
 RL Proteins 19:98-109(1994).
 RN [14]
 RP STRUCTURE BY NMR OF 101-269.
 RX MEDLINE=98145213; PubMed=9484219; DOI=10.1021/bi972181w;
 RA Moy F.J., Chanda P.K., Cosmi S., Pisano M.R., Urbano C., Wilhelm J.,
 RA Powers R.;
 RT "High-resolution solution structure of the inhibitor-free catalytic
 RT fragment of human fibroblast collagenase determined by
 RT multidimensional NMR.";
 RL Biochemistry 37:1495-1504(1998).
 CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
 CC the helical domain. Also cleaves collagens of types VII and X.
 CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
 CC collagen. Cleavage of the triple helix of collagen at about three-
 CC quarters of the length of the molecule from the N-terminus, at
 CC 775-Gly-|-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
 CC substrates and alpha-macroglobulins at bonds where P1' is a
 CC hydrophobic residue.
 CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit.
 CC -1- ENZYME REGULATION: Can be activated without removal of the
 CC activation peptide.
 CC -1- DOMAIN: There are two distinct domains in this protein; the
 CC catalytic N-terminal, and the C-terminal which is involved in
 CC substrate specificity and in binding TIMP (tissue inhibitor of
 CC metalloproteinases).
 CC -1- PTM: Undergoes autocatalytic cleavage to two major forms (22 kDa and
 CC 27 kDa). A minor form (25 kDa) is the glycosylated form of the 22
 CC kDa form. The 27 kDa form has no activity while the 22/25 kDa form
 CC can act as activator for collagenase.
 CC -1- SIMILARITY: Belongs to the peptidase M10A family.
 CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
 CC -----
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X05231; CAA28858.1; -.


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FT METAL 329 329 similarity).
FT Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 378 378 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 427 427 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT DISULFID 278 466 By similarity.
FT CARBOHYD 120 120 N-linked (GlcNAc...) (Potential).
FT CONFLICT 22 23 AT -> FP (in Ref. 2).
FT CONFLICT 30 30 D -> L (in Ref. 2).
FT CONFLICT 35 36 KK -> LL (in Ref. 2).
FT CONFLICT 85 85 N -> F (in Ref. 2).
FT CONFLICT 106 108 KSC -> NPR (in Ref. 2).
FT CONFLICT 113 113 N -> D (in Ref. 2).
SQ SEQUENCE 469 AA; 53354 MW; BAA5504CE24BD7B5 CRC64;

Query Match 71.08; Score 218; DB 1; Length 469;
Best Local Similarity 70.94; Pred. No. 2.6e-18;
Matches 39; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 MQRFGLVNTGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
Db 67 MQRFGLVNTGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 121

RESULT 8
MM01_RANCA STANDARD; PRT; 384 AA.
ID MM01_RANCA
AC Q1133;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Interstitial collagenase precursor (EC 3.4.24.7) (Matrix
DE metalloproteinase-1) (MMP-1) (TCL).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN 1;
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX Medline=95071832; Pubmed=7981043;
RA Oofusa K., Yomori S., Yoshizato K.;
RT "Regionally and hormonally regulated expression of genes of collagen
RT and collagenase in the anuran larval skin.";
RL Int. J. Dev. Biol. 38:345-350(1994).
CC -1- FUNCTION: Cleaves collagens of types I, II, and III at one site in
CC the helical domain. Also cleaves collagens of types VII and X.
CC -1- CATALYTIC ACTIVITY: Cleaves preferentially one bond in native
CC collagen. Cleavage of the triple helix of collagen at about three-
CC quarters of the length of the molecule from the N-terminus, at
CC 775-Gly-Ile-776 in the alpha-1(I) chain. Cleaves synthetic
CC substrates and alpha-macroglobulins at bonds where P1' is a
CC hydrophobic residue.
CC -1- COFACTOR: Binds 2 zinc ions and 4 calcium ions per subunit (By
CC similarity).
CC -1- ENZYME REGULATION: Can be activated without removal of the
CC activation peptide (By similarity).
CC -1- SIMILARITY: Belongs to the peptidase M10A family.
CC -1- SIMILARITY: Contains 1 hemopexin-like domain.
CC -----
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL; S75623; AAB32661.1; -.
DR PIR; I51267; I51267.
DR HSSP; P21692; 1FBL.

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DR MEROPS; M10.001; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 2.
DR Pfam; PF00413; Peptidase_M10; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HK; 2.
DR SMART; SM00235; ZmC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR PROSITE; PS00024; HEMOPEXIN; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc; Zymogen.
FT SIGNAL 1 25 Potential.
FT PROPEP 26 88 Activation peptide (Potential).
FT CHAIN 89 384 Interstitial collagenase.
FT DOMAIN 239 384 Hemopexin-like.
FT SITE 81 81 Cysteine switch (Potential).
FT METAL 113 113 Calcium 1 (By similarity).
FT METAL 129 129 Calcium 2 (By similarity).
FT METAL 139 139 Zinc 1 (By similarity).
FT METAL 141 141 Zinc 1 (By similarity).
FT METAL 146 146 Calcium 3 (By similarity).
FT METAL 147 147 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 149 149 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 151 151 Calcium 3 (via carbonyl oxygen) (By
FT similarity).
FT METAL 154 154 Zinc 1 (By similarity).
FT METAL 161 161 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 163 163 Calcium 2 (via carbonyl oxygen) (By
FT similarity).
FT METAL 165 165 Calcium 2 (By similarity).
FT METAL 167 167 Zinc 1 (By similarity).
FT METAL 169 169 Calcium 3 (By similarity).
FT METAL 170 170 Calcium 1 (By similarity).
FT METAL 172 172 Calcium 3 (By similarity).
FT METAL 189 189 Zinc 2 (catalytic) (By similarity).
FT ACT_SITE 190 190 By similarity.
FT METAL 193 193 Zinc 2 (catalytic) (By similarity).
FT METAL 199 199 Zinc 2 (catalytic) (By similarity).
FT METAL 249 249 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 277 277 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT METAL 347 347 Calcium 4 (via carbonyl oxygen) (By
FT similarity).
FT DISULFID 242 381 By similarity.
SQ SEQUENCE 384 AA; 43582 MW; A5B5E2FB32239DF CRC64;

Query Match 65.6%; Score 201.5; DB 1; Length 384;
Best Local Similarity 65.5%; Pred. No. 2.3e-16;
Matches 36; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MQRFGLVNTGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 55
Db 57 LKQFFGLVNTGKPNNEETLDMKKPRCGVPSGGFMLTPGNPKWERTNLTIRNY 110

RESULT 9
Q8C209 PRELIMINARY; PRT; 465 AA.
AC Q8C209;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus B6-derived CD11 +ve dendritic cells cDNA, RIKEN full-

```


RA Konno H., Akiyama J., Nishi K., Kitsuunai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Mishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
RT "RIKEN Integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771 (2000).
RN [6].
RN
RC SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J;
RR
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hasehizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kanokawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saiboh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Saitoh K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.,
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK089381; BAC40862.1; -.
DR HSSP; P22894; 1JAP.
DR
DR MGD; MGI:1202395; Mmp8.
DR GO; GO:0005615; C:extracellular space; TAS.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZINC; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN1.
SO SEQUENCE 465 AA, 53114 MW, F80522831ACB4B2 CRC64;

Query Match	64.5%	Score 198;	DB 2;	Length 465;
Best Local Similarity	65.5%	Pred. No. 7.7e-16;		
Matches 36;	Conservative	7;	Mismatches 12;	Indels 0;
				Gaps 0;

Qy 1 M Q R F F G L N V T G K P N E E T I D W M K K P C G V P D S G G F M L T P G N P K V E R T N L T Y I R N Y 55
| | | | | : : : : :
Db 66 M O R F F S A E T G K L D A A T M G M E M P C G V P D S G D F L T P G S P K W H T N L T Y I I N H 120
| | | | | : : : : :

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RESULT 11
Q6Y4Q5
ID Q6Y4Q5 PRELIMINARY; PRT; 478 AA.
AC Q6Y4Q5;
DT 05-JUL-2004 (T=EMBLrel. 27, Created)
DT 05-JUL-2004 (T=EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T=EMBLrel. 27, Last annotation update)
DE Stromelysin 1.
GN Name=WMF3;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
[1]
SEQUENCE FROM N.A.
RP
RC TISSUE=Sarcoma;
RA Sorensen K.C., Balkin R.G., Kitchell B.E., Siegel A.M., Schaeffer D.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBEJ databases.
DR EMBL; AV183143; AAC063580.1; -.
DR HSSP; P08254; 1B3D.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.

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GO; GO:0004222; F-metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P-proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase_M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGBD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; Peptidase M10_N; 1.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZnMG; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN_1.
SQ SEQUENCE 478 AA; 53633 MW; 5D1B9DA9D57BC041 CRC64;

Query Match 64.5%; Score 198; DB 2; Length 478;
Best Local Similarity 63.8%; Pred.No.8e-16;
Matches 35; Conservative 7; Mismatches 13; Indels 0; Gaps 0;

QY 1 MQRFGLVNTVGKNEETLDMKKPCGVPDSGFMLTPGNPKWERTNLTYSRNY 55
||| ||| ||| : ||| ::||| ||| ||| ||| ||| |||
DB 67 MQFGLGVTKGVSDTLAMRRPCCGVPDVGDTTFPGMPKWRTHTLYRMNY 121

RESULT 12

ID MM13 XENLA STANDARD; PRT; 469 AA.

AC Q10835; DB 2; Length 478;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Collagenase 3 precursor (EC 3.4.24.-) (Matrix metalloproteinase-L3)
DE (MWP-13) (Fragment).
GN Name=MWP13;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355,
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Tail;
RA Fini M.E., Scott S., Wang Z., Brown D.D.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: Degrades collagen type I.
CC -! COFACTOR: Binds 2 zinc ions and 5 calcium ions per subunit (By similarity).
CC -! DEVELOPMENTAL STAGE: Up-regulated by thyroid hormone in tadpoles during tail resorption.
CC -! MISCELLANEOUS: The Xenopus genome contains two genes coding for very similar enzymes: MWP-13 and MWP-13A.
CC -! SIMILARITY: Belongs to the peptidase M10A family.
CC -! SIMILARITY: Contains 1 hemopexin-like domain.

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CC ENBL; L49412; AAB3996.1; -.
DR HSSP; P33435; 1CXV.
DR MEROPS; M10.013; -.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR006026; Peptidase_M.
DR Pfam; PF00045; Hemopexin; 4.
DR Pfam; PF00413; Peptidase M10; 1.

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DR Pfam; PF03933; Peptidase M10_N; 1.
DR PRINTS; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; 1.
KW Calcium-binding; Collagen degradation; Extracellular matrix;
KW Glycoprotein; Hydrolase; Metal-binding; Metalloprotease; Signal; Zinc;
KW Zymogen.
FT METAL 1 1
FT NON TER <1 17
FT SIGNAL 18 100
FT PROPEP 18 100
FT CHAIN 101 469
FT DOMAIN 279 469
FT SITE 94 94
FT METAL 160 160
FT METAL 170 170
FT METAL 172 172
FT METAL 177 177
FT METAL 178 178
FT METAL 185 185
FT METAL 192 192
FT METAL 194 194
FT METAL 196 196
FT METAL 198 198
FT METAL 203 203
FT METAL 220 220
FT ACT SITE 221 221
FT METAL 224 224
FT METAL 230 230
FT METAL 289 289
FT METAL 291 291
FT METAL 333 333
FT METAL 335 335
FT METAL 381 381
FT METAL 383 383
FT METAL 430 430
FT METAL 432 432
FT DISULFID 282 469
FT CARBOHYD 115 115
FT CARBOHYD 150 150
SQ SEQUENCE 469 AA; EF02BF4BEC429D77 CRC64;

Query Match 63.8%; Score 196; DB 1; Length 469;
Best Local Similarity 67.3%; Pred. No. 1.4e-15;
Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 69 MQSFFGLVTKLNEETLDMKKPRCGVDPDGGVYFFPRKLGWRNLTIRVNY 123

RESULT 13
O93342 PRELIMINARY; PRT; 472 AA.
AC O93342
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase.
OS Gallus gallus (Chicken).

Query Match 63.8%; Score 196; DB 1; Length 469;
Best Local Similarity 67.3%; Pred. No. 1.4e-15;
Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 69 MQSFFGLVTKLNEETLDMKKPRCGVDPDGGVYFFPRKLGWRNLTIRVNY 123

RESULT 13
O93342 PRELIMINARY; PRT; 472 AA.
AC O93342
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Matrix metalloproteinase.
OS Gallus gallus (Chicken).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang M., Kurkinen M.;
RT "Cloning of a novel matrix metalloproteinase (MMP) from chicken
RT embryo fibroblasts.";
RL J. Biol. Chem. 0:0-0(1998).
DR EMBL; AF062392; AAC33733.1; -.
DR HSSP; P45452; 830C.
DR MEROPS; M10.027; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.
DR Pfam; PF00045; Hemopexin; 4.
DR PRINTS; PR03933; Peptidase M10_N; 1.
DR SMART; PR00138; MATRIXIN.
DR SMART; SM00120; HX; 4.
DR SMART; SM00235; ZmMC; 1.
DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
DR PROSITE; PS00024; HEMOPEXIN; 1.
DR PROSITE; PS00142; ZINC PROTEASE; UNKNOWN 1.
SQ SEQUENCE 472 AA; 53254 MW; AAL35CB3F67C868 CRC64;

Query Match 63.8%; Score 196; DB 2; Length 472;
Best Local Similarity 69.1%; Pred. No. 1.4e-15;
Matches 38; Conservative 6; Mismatches 9; Indels 2; Gaps 1;

QY 1 MQRFFGLNVTGKNEETLDMKKPRCGVDPDGGFMLTPGNPKWERTNLTIRNY 55
Db 72 MQRFFGLKVTGKPDTEETLEMMKKPRCGVDPDGLYGVTL-LPGMKNNLTIRVNY 124

RESULT 14
Q10833 PRELIMINARY; PRT; 472 AA.
ID Q10833
AC Q10833
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Collagenase-3.
GN Name=Gene A;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96312514; PubMed=8700860; DOI=10.1073/pnas.93.5.1924;
RA Brown D.D., Wang Z., Furrow J.D., Kanamori A., Schwartzman R.A.,
RA Remo B.F., Pinder A.;
RT "The thyroid hormone-induced tail resorption program during Xenopus
RT laevis metamorphosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:1924-1929(1996).
DR EMBL; UA1824; AAC59870.1; -.
DR HSSP; P33435; 1CXV.
DR MEROPS; M10.013; -.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000585; Hemopexin.
DR InterPro; IPR006026; Peptidase M.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR009070; PGSD_like.

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DR Pfam; PF00045; Hemopexin; 4.
 DR Pfam; PF03933; Peptidase M10_N; 1.
 DR PRINTS; PR00138; MATRXIN.
 DR SMART; SM00120; HX; 4.
 DR SMART; SM00235; Zmc; 1.
 DR PROSITE; PS00546; CYSTEINE SWITCH; 1.
 DR PROSITE; PS00024; HEMOPEXIN; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Collagen.
 SQ SEQUENCE 472 AA; 53837 MW; CDF490F5738593B4 CRC64;
 Query Match 63.8%; Score 196; DB 2; Length 472;
 Best Local Similarity 67.3%; Pred. No. 1.4e-15;
 Matches 37; Conservative 4; Mismatches 14; Indels 0; Gaps 0;
 QY 1 MQRFFGLVNTGKNEETLDMMKPRCGVPSGGFPLTPGNPKWERTNLTIRINY 55
 DB 72 MQSFFGLEVTGKNEETLDMMKPRCGVPSGGFPLTPGNPKWERTNLTIRINY 126
 RESULT 15
 MM03 HUMAN
 ID MM03 HUMAN STANDARD; PRT; 477 AA.
 AC P08254;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Stromelysin-1 precursor (EC 3.4.24.17) (Matrix metalloproteinase-3)
 DE (MMP-3) (Transin-1) (SL-1).
 GN Names=MMP3; Synonym=STMY1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 [1]
 RN
 SEQUENCE FROM N.A., AND SEQUENCE OF 18-24.
 RX MEDLINE=88198243; PubMed=3360803;
 RA Saus J., Quinones S., Otani Y., Nagase H., Harris E.D. Jr.,
 RA Kurkinen M.;
 RT "The complete primary structure of human matrix metalloproteinase-3.
 RT Identity with Stromelysin.";
 RL J. Biol. Chem. 263:6742-6745 (1988).
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 RN
 SEQUENCE FROM N.A.
 RC TISSUE=Fibroblast;
 RX MEDLINE=87156645; PubMed=3030290;
 RA Whitam S.E., Murphy G., Angel P., Rahmsdorf H.J., Smith B., Lyons A.,
 RA Harris T.J.R., Reynolds J.J., Herrlich P., Docherty A.J.P.;
 RT "Comparison of human Stromelysin and collagenase by cloning and
 RT sequence analysis.";
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 RN
 SEQUENCE FROM N.A.
 RX MEDLINE=88016164; PubMed=3477804;
 RA Wilhelm S.M., Collier I.E., Kronberger A., Eisen A.Z., Marner B.L.,
 RA Grant G.A., Bauer E.A., Goldberg G.I.;
 RT "Human skin fibroblast Stromelysin: structure, glycosylation,
 RT substrate specificity, and differential expression in normal and
 RT tumorigenic cells.";
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 RN
 SEQUENCE FROM N.A.
 RA Lin D., Duncan M., Allen E., Araujo R., Aparicio A., Chai A.,
 RA Chung E., Davis K., Federspiel N., Hyman R., Kalman S., Komp C.,
 RA Kurd O., Lashkari D., Lew H., Namath A., Oefner P., Roberts D.,
 RA Heller R., Davis R.W.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
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 RN
 SEQUENCE FROM N.A., AND VARIANT GLU-45.
 RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
 RA Nickerson D.A.;
 RT "SeattlesNP. NHLBI HU66682 program for genomic applications, UW-
 RT FHCR, Seattle, WA (URL: <http://pga.gs.washington.edu>).";

RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
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 RN
 ZMOGEN ACTIVATION
 RX MEDLINE=90344802; PubMed=2383557;
 RA Nagase H., Englund J.J., Suzuki K., Salvesen G.;
 RT "Stepwise activation mechanisms of the precursor of matrix
 RT metalloproteinase 3 (stromelysin) by proteinases and (4-
 RT aminophenyl)mercuric acetate.";
 RL Biochemistry 29:5783-5789 (1990).
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 RN
 STRUCTURE BY NMR OF CATALYTIC DOMAIN.
 RX MEDLINE=95384761; PubMed=7656014;
 RA Gooley P.R., O'Connell J.P., Marcy A.I., Cuca G.C., Salowe S.P.,
 RA Bush B.L., Hermes J.D., Esser C.K., Hagmann W.K., Springer J.P.,
 RA Johnson B.A.;
 RT "The NMR structure of the inhibited catalytic domain of human
 RT Stromelysin-1.";
 RL Nat. Struct. Biol. 1:111-118 (1994).
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 RN
 STRUCTURE BY NMR OF 100-267.
 RX MEDLINE=99043696; PubMed=9827994;
 RA Stockman B.J., Waldon D.J., Gates J.A., Scallion T.A.,
 RA Kloosterman D.A., Mizsak S.A., Jacobsen E.J., Belonga K.L.,
 RA Mitchell M.A., Mao B., Petke J.D., Goodman L., Powers E.A.,
 RA Ledbetter S.R., Kayes P.S., Vogeli G., Marshall V.P., Petzold G.L.,
 RA Poorman R.A.;
 RT "Solution structures of Stromelysin complexed to thiazole
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 RN
 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 18-272.
 RX MEDLINE=96117647; PubMed=8535233;
 RA Becker J.W., Marcy A.I., Rokosz L.L., Axel M.G., Burbaum J.J.,
 RA Fitzgerald P.M.D., Cameron P.M., Esser C.K., Hagmann W.K.,
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 RT "Stromelysin-1: three-dimensional structure of the inhibited catalytic
 RT domain and of the C-truncated proenzyme.";
 RL Protein Sci. 4:1966-1976 (1995).
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 RN
 X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 100-266
 RX MEDLINE=96311273; PubMed=8740360; DOI=10.1016/S0969-2126(96)00043-3;
 RA Dhanaraj V., Ye Q.-Z., Johnson L.L., Hupe D.J., Otwine D.F.,
 RA Dunbar J.B. Jr., Rubin J.R., Pavlovsky A., Humblet C., Blundell T.L.;
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 RT catalytic domain and its comparison with members of the zinc
 RT metalloproteinase superfamily.";
 RL Structure 4:375-386 (1996).
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 RN
 X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 105-264.
 RX MEDLINE=97236965; PubMed=9083493; DOI=10.1021/jm960465t;
 RA Esser C.K., Bugianesi R.L., Caldwell C.G., Chapman K.T., Durette P.L.,
 RA Girotta N.N., Kopka I.E., Lanza T.J., LeVorse D.A., Maccoss M.,
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 RX MEDLINE=97433330; PubMed=9288970; DOI=10.1038/37995;
 RA Gomis-Rueth F.-X., Maskos K., Betz M., Bergner A., Huber R.,
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 RA Bartunik H., Bode W.;
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 RL Nature 389:77-81 (1997).
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 RN
 X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 100-264.
 RX MEDLINE=99006562; PubMed=9792098;
 RA Finzel B.C., Baldwin E.T., Bryant G.L. Jr., Hess G.F., Wilks J.W.,

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DR  PDB; 1QIA; X-ray; A/B/C/D=106-267.
DR  PDB; 1QIC; X-ray; A/B/C/D=106-266.
DR  PDB; 1SLW; X-ray; @=18-272.

Query Match      63.8%; Score 196; DB 1; Length 477;
Best Local Similarity 63.6%; Pred. No. 1.4e-15;
Matches 35; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

Qy  1  MQRFFGLVNTGKNEETLDMKKKPRGCVDPDGGFMLTGPNPKWERTNLTYYRNY 55
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Db  67  MQRFLGLVNTGKDSLTLEWRKPRGCVDPDGHFRTPPGIGPKWKTHLTYYRNY 121
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